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6, 2004, 15:59:10 ; Search time 40 Seconds (without alignments) 353.167 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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MERVTLALLILAGLTALEAN.......HSPVPEKAIPLITPGSATTC
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SUMMARIES

구	Human kidney dises	Human signal nenti	Membrane-bound nro	Human PRO nolyment	Himan DBO1069	Human PRO1069 (170)	Sporteted		Human secreted pol
QI	AAY85679	AAY87258	AAY66705	AAU29123	AAB87550	AAB65228	ABG95875	ABU71211	ABU71530
DB 	21	21	21	22	22	22	23	24	24
ery cch Length DB	89	89	89	68	89	89	68	8 8	89
sch :	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Yue H;

Klingler TM, Azimzai Y,

Walker MG, Volkmuth W,

WPI; 2000-665116/64. N-PSDB; AAC66135.

Novel hum	Human PRO	Ø	Ä	_		,4	_		C	ρ p			W		Human PRO			23	0		, c	D of	HIF	9	~		Human MAT		u	br	Ö	O	ч	re	
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ALIGNMENTS

Nephrotropic; cytostatic; human; kidney disease associated; hyper Bartter's syndrome; Gitelman syndrome; nephrolithiasis; renal fairenal amyloidosis; primary aldosteronism; Addison's disease; canc glomerulonephritis; dysplastic malformation; medullary cystic dismedullary sponge kidney; tubular dysplasia; Alport's syndrome. Human kidney disease associated protein SEQ ID 11. AAY85679 standard; Protein; 89 AA. 28-MAR-2000; 2000WO-US08260. (first entry) (INCY-) INCYTE PHARM INC. WO200061622-A2. Homo sapiens. 09-APR-1999; 13-FEB-2001 19-OCT-2000 AAY85679; RESULT 1 AAY85679

'disease associated gene useful for diagnosing treating and enal disorders, is uromodulin, NKCC2, NCCT, aldolase B, il, PDZK1, NPT1, calbindin, kininogen or CIC-Kb

e 35-36; 36pp; English.

des AAC66131-C66139 represent human kidney disease enes. Proteins AAY85678-Y85680 represent human kidney disease proteins The polymuclectides have nephrorropic and cytostatic polymuclectides, are nephrorropic and cytostatic is containing them are useful for diagnosing, prognosing, l preventing renal disorders such as Barter's syndrome, alrome, autosemal dominant polycystic kidney for identifying is. The genes and proteins are also useful for identifying ithat are associated with a specific disease, regulatory cellular compartment, cell type, tissue type or species, ful in diagnosis, prognosis, treatment and evaluation of trens and diseases for e.g. renal amyloidoels, hypertension, streronism, Addison's disease, renal failure, hyperitis chronic glomerulomephritis, tubulointerstitial ystic disorders and dysplastic malformations, inherited enal disease (RRD), medullary cystic disease, medullary y and tubular dysplastic malformatione, multiple nanhary energy and tubular dysplasia, Alport's syndrome, non-renal nanhary energy. nephrotoxic disorders.

0 VTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 60 VTLALLILLAGITALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 60 0; Gaps Length 89; 0; Indels 100.0%; Score 461; DB 21; 100.0%; Pred. No. 1.2e-50; 0; Mismatches Conservative

KSSQKQHSPVPEKAIPLITPGSATTC 89 KSSOKOHSPVPEKAIPLITPGSATTC 89

ndard; Protein; 89 AA

(first entry)

peptide containing protein HSPP-35 SEQ ID NO:35.

l peptide-containing protein; HSPP; diagnosis; cancer; cardiovascular disease; anticancer; anti-inflammatory; noctropic; neuroprotective; cardiovascular; hegatotropic; gene therapy; cell proliferation; neurological disorder; disorder; developmental disorder; arteriosclerosis; soriasis; acquired immune deficiency syndrome; anaemia; n's disease; infection; Altheimer's disease; schizophrenia; disease; Huntington's disease; ovulatory defect;

99WO-US14484. 98US-0090762, 98US-0094983 98US-0102686.

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AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent human signal peptide-containing proteins HSPP-1 to HSPP-134. HSI anticancer, anti-inflammatory, antimicrobial, noctropic, hepatot neuroprotective, cardiovascular and antiasthmatic activities, at associated with decreased activity or function of HSPP. Antagon: HSPP associated with decreased activity or function of HSPP. Antagon: associated with decreased activity or function of HSPP. Antagon: activity or function of HSPP. Such diseases include cell prolife (including cancer), inflammation, cardiovascular, neurological, reproductive or developmental disorders, (e.g. arteriosclerosis, cirrhosis, psoriasis, acquired immune deficiency syndrome, anamostic carbomental disorders, parkinson's or Huntington'd diseases, schizophrenia, ovulatory defects, muscular dystrophy) nucleic acids can be used for the recombinant production of HSPP and assay, and amplification assay, and and applification assay.
                                                                            Baughn 1
8. Hill
                                                                                                                                                                                                       New human signal peptide-containing proteins useful in treatment prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis and monitoring), in gene therapy, as antisense, triplex-forming or ribozyme therapeutics, for detecting related or genetic variations, and for chromosomal mapping. HSPP are algraise specific antibodies (Ab) and to screen for agonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antagonists (potential therapeutic agents). Ab are used to diagramultic. HSPP-related diseases (in usual immunoassays), as there antagonists, in competitive drug screens, and for purification of from natural sources.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MERVILALLLAGLTALEANDPFANKDDPFYYDWKNLOLSGLICGGLLAIAGIAA
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                                                                      Gorgone GA, Corley NC, Guegler KJ, Ba
foung J, Yue H, Patterson C, Reddy R,
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                                                                                                                                                                                                                                                                                 Claim 1; Page 182; 327pp; English.
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 98US-0112129,
                                                                                          Au-Young J,
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11-DEC-1998;
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Membrane-bound polypeptide, PRO polypeptide, LDL receptor, TIE l pharmaceutical, receptor immunoadhesin, gene mapping. Homo sapiens.

WO9963088-AZ.

		1998; 98US-0055929. 1998; 98US-0056112. 1998; 98US-0056143. 1998; 98US-0056143. 1998; 98US-00561329. 1998; 98US-0056766. 1998; 98US-0056761. 1998; 98US-0056791. 1998; 98US-0056891. 1998; 98US-0056891. 1998; 98US-0056892. 1998; 98US-0056892. 1998; 98US-0056892. 1998; 98US-0056892. 1998; 98US-0056892. 1998; 98US-0056860. 1998; 98US-0056860. 1998; 98US-0056860.	998; 998; 998; 998; 998; 998; ENENT
000000000000000000000000000000000000000) O O O O O O O O O O O O O O O O O O O	PR 10-AUG-1998 PR 11-AUG-1998 PR 11-AUG-1998 PR 11-AUG-1998 PR 17-AUG-1998 PR 18-AUG-1998	20-AUG-1 26-AUG-1 26-AUG-1 26-AUG-1 26-AUG-1 26-AUG-1 26-AUG-1 26-AUG-1 26-AUG-1 26-AUG-1 26-AUG-1 26-AUG-1 116-SEP-1 116-SEP-1 12-JAN-1 12-JAN-1 12-JAN-1 Baker K,
99WO-US12252. 98US-0037607. 98US-0087609. 98US-0087759. 98US-0087827. 98US-0088021. 98US-0088028. 98US-0088028.	99US-0088033. 99US-008326. 99US-0088167. 99US-008812. 99US-008812. 99US-008872. 99US-008872. 99US-008872. 99US-008874. 99US-008874. 99US-008874. 99US-008874. 99US-008874. 99US-008874.	98US-0088828. 98US-0088828. 98US-0088861. 98US-0088861. 98US-0088863. 98US-0089090. 98US-0089140. 98US-0089514. 98US-0089532. 98US-0089532. 98US-0089532. 98US-0089533. 98US-0089533. 98US-0089530. 98US-0089530. 98US-0089530. 98US-0089590.	802-0090245. 803-0090254. 803-0090254. 803-0090254. 803-0090349. 803-0090429. 803-0090444. 803-0090444. 803-0090445. 803-0090445. 803-0090535. 803-0090536. 803-0090546.

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des encoding them. The PRO sequences of the invention were des encoding them. The PRO sequences of the invention were ased on extracellular domain homology screening. The PRO we homology with proteins including LDL receptors, TIE various enzymes. The membrane-bound proteins and receptor e useful as pharmaceutical and diagnostic agents to block and interactions. The membrane-bound proteins can also be screening of potential peptide or small molecule inhibitors and receptor/ligand interaction. The PRO encoding sequences hybridization probes, in chromosome and gene mapping and in of antisense RNA and DNA. PRO nucleic acid sequences useful for the preparation of PRO polypeptides, especially
ind proteins and related nucleotide sequences
                                                                                          g 180; 822pp; English.
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9 AA;

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                                                                                                                                               VTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLLCGGLLAIAGIAAVLSGK 60
                                                                                                 VTLALLILLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK
                                                     0; Gaps
100.0%; Score 461; DB 21; Length 89; 100.0%; Pred. No. 1.2e-50; ive 0; Mismatches 0; Indels C
                                                   Conservative
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89 KSSQKQHSPVPEKAIPLITPGSATTC 89 KSSQKQHSPVPEKAIPLITPGSATTC

ndard; Protein; 89 AA.

(first entry)

lypeptide sequence #100.

ide, mammal, tumour, cancer, human, cattle, horse, sheep;
3; goat, rabbit, tumour necrosis factor alpha; TNF-alpha;
rocyte cell; cell proliferation; cell differentiation, colon;
3; breast; prostate, rectum; cervix; liver; genetic disorder.

2000WO-US05601. 2000WO-US05841. 2000US-187202P. 2000US-191048P. 2000US-191314P. 2000US-192655P. 2000US-186968P. 2000US-189320P. 2001WO-US06520 2000US-189328P 2000US-190828P. 2000US-191007P. 2000WO-US06884

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29-MAR-2000; 2000US-193032P.
39-MAR-2000; 2000WG-193053P.
39-MAR-2000; 2000WG-193053P.
44-APR-2000; 2000US-194647P.
44-APR-2000; 2000US-19669P.
44-APR-2000; 2000US-19669P.
44-APR-2000; 2000US-19669P.
44-APR-2000; 2000US-19669P.
44-APR-2000; 2000US-19669P.
48-APR-2000; 2000US-19669P.
48-APR-2000; 2000US-199654P.
48-APR-2000; 2000US-199654P.
48-APR-2000; 2000US-199654P.
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48-APR-2000; 2000US-199654P.
48-APR-2000; 2000US-199654P.
48-APR-2000; 2000WG-1914042.
48-APR-2000; 2000WG-1914042.
48-AUG-2000; 2000WG-1914941.
48-AUG-2000; 2000WG-1914941.
48-AUG-2000; 2000WG-191328.
48-AUG-2000; 2000WG-193328.
48-AUG-2000; 2000WG-193328.
48-AUG-2000; 2000WG-193328.
48-AUG-2000; 2000WG-1933328.
48-AUG-2000; 2000WG-1933328.
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(GETH) GENENTECH INC.

Godowski PJ, Gurr Goddard A, Godor ood WI, Zhang Z; Desnoyers L, Goudan-Chen J, Desuci. ... v. Watanabe CK, Smith V, Baker KP, Pan J,

WPI; 2001-602746/68. N-PSDB; AAS46024. Novel nucleic acids encoding PRO polypeptides, used to diagnose presence of tumours, such as prostate and breast tumours, in man to screen for modulators of the compounds -

Claim 11; Fig 200; 774pp; English.

Sequences AAU29024-AAU29328 represent PRO polypeptides of the in The PRO polypeptides and their associated nucleic acids can be undetect the presence of a tumour in a mammal by comparing the levex expression of a PRO polypeptide in a test sample of cells from the and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human when contacted with it. A specific polypeptide can be used to be proliferation of chondrocyte cells. The P proteins can be used to determine the presence of tumours and all contacting the under development, particularly adversal, lung the profits the total procession of the proliferation of chondrocyte cells. The P conteins can be used to determine the presence of tumours and all contacting the profits of the proliferation of the proliferation of the proliferation of the proliferation of contacting the procession of the proliferation of the prol breast, prostate, rectal, cervical, or liver tumours, in mammali subjects. The oligonucleotide probes specific for the PRO nuclei can be used for genetic analysis of individuals with genetic dis-

89 AA; Sequence

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1 MERVILALLILAGLIALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAA
                                           ;
100.0%; Score 461; DB 22; Length 89; 100.0%; Pred. No. 1.2e-50; cive 0; Mismatches 0; Indels (
                    Local Similarity 100.
les 89; Conservative
  Query Match
                                   Matches
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1 MERVILALLILAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAA'

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(GETH) GENENTECH INC. WPI; 2001-032160/04. N-PSDB; AAF44191. WO200073454-A1. Homo sapiens. 05-JAN-2000; 11-FEB-2000; 02-MAR-2000; 15-MAR-2000; 22-FEB-2000; 24-FEB-2000; 02-APR-2001 07-DEC-2000 28-JUL-1999 .6-DEC-1999; AAB65228; Roy MA, Zhang Z; AAB65228 equence is a human PRO polypeptide (secreted and the PRO protein, and PRO agonists, PRO antagonists or sodies are useful for preparation of a medicament useful in of a condition which is responsive to the PRO protein, agonists or anti-PRO antibodies. The PRO protein may also be blecular weight markers for protein electrophoresis. The PRO protein are has applications in molecular biology, including use as probes, and in chromosome and gene mapping. 09 CLALLLIAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 60 TLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 0; Gaps Goddard A, Godowski PJ; Wood WI; ucleic acids encoding PRO polypeptides, useful in logy, including use as hybridization probes, and in 100.0%; Score 461; DB 22; Length 89; 100.0%; Pred. No. 1.2e-50; ive 0; Mismatches 0; Indels SSOKOHSPVPEKAIPLITPGSATTC 89 SSQKQHSPVPEKAIPLITPGSATTC 89 Gerritsen ME, Watanabe CK, dard; Protein; 89 AA. 50; 278pp; English.

gene mapping.

onservative

99WO-US21090. 99US-0169495. 99US-0170262.

2000WO-US23328

otein; mapping

(first entry)

2000WO-US04341. 2000WO-US04342.

2000US-0187202 2000US-0199397 0000WO-US14042

2000US-0209832

Gurney AL,

260/18.

lvaroff E, PECH INC.

2000WO-US05601

2000US-0175481

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The present invention describes human secreted and transmembrane proteins. The PRO proteins have cytostatic activity. The PRO protean be used for targeted delivery of bioactive molecules, such as team be, radiolabels or antibodies, that cause cell death. PRO nuc sequences, and their fragments, can be used as hybridisation probarmonesomal and gene mapping, and in the generation of anti-sense and DNA. They may also be used to produce transgenic animals which used to develop and screen therapeutically useful reagents. The Protectide and protein sequence can be used for tissue typing and
                                                                                                   Human; secreted and transmembrane protein; PRO; cytostatic; cell death; cancer; chromosomal mapping; gene mapping; tissue tygidagnostic assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baker KP, Botstein D, Desnoyers L, Eaton DL; and S, Gerber H, Gerriteen ME, Goddard A, Godows Gurney AL, Rijavin IJ, Napler MA, Pan J, Beonirt TA, Tumas D, Watanabe CK, Williams PM, Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death -
                                                                           Human PRO1069 (JNQ526) protein sequence SEQ ID NO:262.
AAB65228 standard; Protein; 89 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Fig 180; 935pp; English.
                                                                                                                                                                                                                                                           99WO-US12252.
99US-0141037.
99US-0144048.
99US-0144758.
99US-014622.
99US-014622.
99WO-US21090.
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99WO-US28313
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99WO-US30095
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2000WO-US06884
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Ashkenazi AJ, Ban.
Talanay AL, F
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ncer. Anti-PRO antibodies can be used in diagnostic assays. AAF4470 represent PCR primers and hybridisation probes used thion of human PRO sequences. AAF44087 to AAF44269 and AAB65300 represent human PRO polynucleotide and protein ven in the exemplification of the present invention.

AA;

VTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 60 VTLALLILLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLIAIAGIAAVLSGK 60 Gaps . 0 Length 0; Indels 100.0%; Score 461; DB 22; 100.0%; Pred. No. 1.2e-50; 0; Mismatches Conservative larity

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KSSQKQHSPVPEKAIPLITPGSATTC 89 KSSÓKQHSPVPEKAIPLITPGSATTC 89

ndard; Protein; 89 AA.

ed/transmembrane protein PRO1069.

ted protein; transmembrane protein; antirheumatic;
c; osteopathic; sports-related joint problem;
rtilage defect; osteoarthritis; rheumatoid arthritis.

2001US-0006867

98US-082797P. 98US-083495P. 98US-085579P. 98US-088811P. 98US-088824P. 98US-089105P. 98US-089514P. 98US-088825P. 99WO-US30720. 98WO-US19330. 99WO-US12252 99WO-US20111 99WO-US21194. 2000WO-US04342 2000WO-US15264 99WO-US10733 99WO-US21090 2000WO-US04341 2000WO-US08439 2000WO-US23328 2000WO-US14042

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The invention relates to an isolated secreted and transmembrane polypeptide having 80 % sequence identity to a sequence appearize to as AB859851-AB639534 or their associated signal peptide, or a sequence as AB859851-AB639534 or their associated signal peptide, or a sequence as AB859851-AB639534 or their associated signal peptide. Also included the nucleic acids encoding the proteins with their associated signal peptide. Also included the nucleic acids encoding the proteins, vectors, host cells, the proteins are useful for detecting a polypeptide designated as E, F, or D in a sample suspected of containing an A, B, C or D polyper to by contacting the sample with a polypeptide designated as E, F, or or Dil polypeptide conjugate in the sample, where A is a PR01072 polypeptide, B is a PR02011 polypeptide, C is a PR01096 polypeptide, D is a PR01976 polypeptide, T is a PR010976 polypeptide of is a PR010976 polypeptide of is a PR02011 polypeptide. The sample comprises a cell suspected of expressing a detectable label or is attached to a solid support: The protein useful for linking a bioactive molecule to a cell expressing a detectable label or is attached to a solid support: The protein useful for linking a bioactive molecule to a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H or I. The causes death of the cell. A, B, C, D, E, F, G, H, or I or and expressing a polypeptide designated as A, B, C or D or E, F, G, H or I. The causes death of the cell. A, B, C, D, E, F, G, H, or I or adainst them are useful for modulating a biological activity of expressing a polypeptide designated designated as A, B, C or D or E, F, G, H or I. The call is killed. The proteins are useful for identifying aponists or antipagentic or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapeutic useful reagents, for chromosome identification, and therapy. The antibody is useful as a therapeutic agent, in a diacassay and for affinity purification of the protein from recombincell culture natural sources. The present sequence represents a secreted or transmembrane protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       molecular weight markers for protein electrophoresis purposes, a therapeutic agents for treating sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding the proteins are useful as hybridisation in chromosome and gene mapping, in the generation of anti-sense DNA, for the preparation of the proteins, to generate transgenic knockout animals which are useful in the development and screeni
                                                                                                                                                                                                                                                                                                                                 modulating biological activity of a cell, or for treating sports-related joint problems, osteoarthritis or rheumatoid arth
                                                                                                                                                               Godowski PJ
                                                                                                                                                                                                                                                                                                         New isolated secreted and transmembrane PRO polypeptide useful
                                                                                                                                                            Goddard A,
                                                                                                                                                                                    Wood WI;
                                                                                                                                                          Gerritsen ME,
Watanabe CK.
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Fig 50; 399pp; English.
                          2001WO-US21066.
2001WO-US21735.
  20-JUN-2001; 2001WO-US19692
                                                                                                                                                                                    Gurney AL,
                                                                                                                                                          ங்
                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                       Filvaroff
                                                                                                                                                                                                                               WPI; 2002-731348/79.
                                                                                                                                                                               JC,
                          29-JUN-2001;
                                                                                                                                                                                                                                                                                                                                 modulating
                                                                                                                                                                                  Grimaldi
                                                                                                                                                          Eaton
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89 AA; Sequence

1 MERVILALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAN 1 MERVILALLIAGLIALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAN .. Length 89; Indels .. 0 100.0%; Score 461; DB 23; 100.0%; Pred. No. 1.2e-50; Mismatches .. 89; Conservative Local Similarity Query Match **datches** ð 임

89 61 CKYKSSQKQHSPVPEKAIPLITPGSATTC 89 CKYKSSOKOHSPVPEKAIPLITPGSATTC

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2001WO-US06520

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97US - 066466P
97US - 069425P
97US - 069425P
97US - 069425P
97US - 069470P
98US - 0774542P
98US - 0810194P
98US - 081195P
98US - 081195P
98US - 081195P
98US - 081195P
98US - 081414P
98US - 081414P
98US - 081466P
98US - 081414P
98US - 081466P
98US - 081414P
98US - 081466P
98US - 081414P
98US - 081613P
98US - 081612P
98US - 088025P
98US - 088025P
98US - 088012P
98US - 088117P
98US - 088121P
98US - 088117P
98US - 088112P
98US - 088112P
98US - 088112P
98US - 088112P
98US - 088111P
98US - 088111P
98US - 088811P
98US - 088861P
98US - 088861P
221-NOV-1997;
24-NOV-1997;
11-DEC-1997;
12-DEC-1997;
11-DEC-1997;
11-DEC-1997;
11-MAR-1998;
20-MAR-1998;
20-MAR-1998;
21-MAR-1998;
22-MAR-1998;
22-MAR-1998;
23-MAR-1998;
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02-JUN-1998;
03-JUN-1998;
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04-JUN-1998;
04-JUN-1998;
05-JUN-1998;
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05-JUN-1998;
09-JUN-1998;
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12-JUN-1998;
16-JUN-1998;
16-JUN-1998;
17-JUN-1998;
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                                                                                                                                                                                                                                                      ecreted; transmembrane; cytostatic; TNF-alpha; blood; is factor alpha release; chondrocyte cell; proliferation; on; tumour; gene therapy.
                                                                            dard; Protein; 89 AA
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98WO-US19330

98WO-US21141

99WO-US102528

99WO-US102529

99WO-US20111

99WO-US20111

99WO-US28301

99WO-US28301

99WO-US28301

99WO-US28301

99WO-US28301

99WO-US28301

2000WO-US06841

2000WO-US05841

2000WO-US05865

2000WO
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                                                                                                                                                                  (first entry)
                                                                                                                                                                                                             protein.
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New isolated antibody specifically binding a PRO polypeptide, use for the preparation of a medicament for treating disorders with taberrant expression or activity of the PRO polypeptide, such as t conditions and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an antibody that binds to a polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Godowski PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goddard A,
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerritsen ME,
Watanabe CK,
                                                                                                                                                                         Human; gene therapy; tumour; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 117; 406pp; English.
                                                                                                                                       Human secreted polypeptide PRO1069
                               ABU71530 standard; Protein; 89 AA.
                                                                                                                                                                                                                                                                                                                                                                 08-MAR-1999; 99WO-USD502144.
14-MAR-1999; 99WO-USD502138.
13-DEC-2000; 2000WO-USD5174.
18-FEB-2000; 2000WO-USD5131.
21-MAR-2000; 2000WO-USD5132.
22-MAY-2000; 2000WO-USD5132.
22-MAY-2000; 2000WO-USD5132.
22-MAY-2000; 2000WO-USJ326.
24-AUG-2000; 2000WO-USJ326.
25-AUG-2000; 2000WO-USJ326.
25-AUG-1999; 99US-0311832.
25-AUG-1999; 99US-0380139.
25-AUG-2000; 2000US-0644844.
22-AUG-2000; 2000US-0644844.
22-AUG-2000; 2000US-064810.
18-SEP-2000; 2000US-064810.
18-SEP-2000; 2000US-0648280.
30-MAR-2001; 201US-0816744.
10-MAY-2001; 201US-0816744.
10-MAY-2001; 201US-081674.
10-MAY-2001; 201US-0816599.
                                                                                                                                                                                                                                                                                                                                                      98KR-0062142.
99WO-US05028.
99WO-US10733.
99WO-US31274.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUL-2001; 2001US-0908827
06-DEC-2001; 2001US-0006867
                                                                                                  10-JUN-2003 (first entry)
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3, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-330485/31.
N-PSDB; ACA58834.
                                                                                                                                                                                                                                              US2003013855-A1.
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Grimaldi JC,
                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                      30-DEC-1998;
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                                                                 ABU71530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /TLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 461; DB 24; Length 89; arity 100.0%; Pred. No. 1.2e-50; onservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SSOKQHSPVPEKAIPLITPGSATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSOKOHSPVPEKAIPLITPGSATTC
98US - 089528P - 98US - 089528P - 98US - 089528P - 98US - 089528P - 98US - 090246P - 98US - 090246P - 98US - 090246P - 98US - 0904444P - 98US - 0904444P - 98US - 0904444P - 98US - 090688P - 98US - 090689P - 98US - 090689P - 98US - 090689P - 98US - 091528P - 98US - 09179718P - 98US - 09179
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containing antibodies that specification. The methods and containing antibodies that specifically bind a PRO of the present invention are useful for the preparation of a rate treatment of disorders associated with the aberrant activity of the PRO polypeptide, such as tumour conditions hey can also be used to generate transgenic or knockout in the development and screening of therapeutically useful in the Development and encoding nucleic acids can be used as ght markers for protein electrophoresis, chromosome in and tissue typing. The PRO polypeptides are useful to enesis e.g wound healing, in the treatment of sports-related abetes: hyperinsulingeness, osteoarthritis or rheumatoid betes: hyperinsulinaemia and hypoinsulinaemia. The treatment of abetes: hyperinsulinaemia and hypoinsulinaemia. The ty be used in various diagnostic, competitive binding and/or tation assays. The present sequence represents the amino of a PRO polypeptide of the invention.

0; Gaps 100.0%; Score 461; DB 24; Length 89; 100.0%; Pred. No. 1.2e-50; Indels 0; 0; Mismatches onservative

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TLALLLLAGLTALBANDPFPANKDDPPYYDWKNLQLSGLLCGGLLAIAGIAAVLSGK 60

SSOKOHSPVPEKAIPLITPGSATTC 89 SSQKQHSPVPEKAIPLITPGSATTC

lard; Protein; 89 AA.

(first entry)

ecreted and transmembrane protein PRO1069,

ad and transmembrane polypeptide;
9ping; gene mapping; transgenic animal; knockout animal;
Jent screening; chromosome identification; tissue typing;

:002US-0063512.

:001US-0006867.

ECH INC.

Godowski PJ; Goddard A, Wood WI; Gerritsen ME, Watanabe CK,

ind transmembrane PRO polypeptides and nucleic acid oding the polypeptides, useful in gene therapy or dicament for treating a condition that is responsive to eptide or antibody

50; 409pp; English.

describes novel isolated PRO polypeptides. The PRO

polypeptides or anti-PRO antibodies are useful in preparing a me for treating a condition that is responsive to the PRO polypepti antibody. The PRO nucleotide sequences may be used as hybridisat probes in chromosome and gene mapping, or in generating antisens and DNA. PRO nucleic acids are also useful in preparing PRO poly in assays to identify other proteins or molecules involved in bireaction, to generate transgenic animals or knockout animals, who turn are useful in the development and screening of therapeutica cuseful reagents, for chromosome identification, and tissue typin PRO polypeptides and nucleic acid molecules are also useful in githerapy, and as molecular weight markers for protein electrophory purposes. The anti-PRO antibodies may be used in diagnostic assay. PRO, or for the affinity purification of PRO from recombinant ceiculture or natural sources. This is the amino acid sequence of a human secreted and transmembrane PRO poypeptide. 1 MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAN 1 MERVTLALLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAV . 0 Length 89; Indels 100.0%; Score 461; DB 24; 100.0%; Pred. No. 1.2e-50; 0; Mismatches CKYKSSQKQHSPVPEKAIPLITPGSATTC 89 61 CKYKSSOKOHSPVPEKAIPLITPGSATTC 89 Conservative Local Similarity les 89; Conserv 89 AA; Seguence Query Match Matches 5555555555555555×8 δ 셤 ò

RESULT 11

ABU72133 standard; Protein; 89 AA.

13-JUN-2003 (first entry)

Human PRO polypeptide #25.

Human; PRO polypeptide; secreted and transmembrane protein; anti-PRO antibody; diagnostic assay; gene expression.

Homo sapiens.

US2003023042-A1.

30-JAN-2003.

01-MAY-2002; 2002US-0063502.

06-DEC-2001; 2001US-0006867.

(GETH) GENENTECH INC.

Goddard A, Godowski PJ; Wood WI; Gerritsen ME, Watanabe CK, Β, Aľ, Filvaroff Grimaldi JC, Gurney Eaton DL,

WPI; 2003-331484/31. N-PSDB; ACA63397.

Novel monoclonal antibody that binds to secreted and transmembrant polypeptide, useful for detecting and purifying the polypeptide as also for treating conditions responsive to the antibody

The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the treatment of a condition responsive to

varoff E, Gurney AL,

84/31.

Disclosure; Fig 50; 408pp; English.

Conservative larity.

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01-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US34956.
21-DES-2001; 2001WO-US34956.
20-UUN-2001; 2001WO-US17800.
20-UUN-2001; 2001WO-US17800.
29-UUN-2001; 2001WO-US1780.
29-UUN-2001; 2001WO-US1780.
29-UUN-2001; 2001WO-US1785.
29-UUN-2001; 2001WO-US1785.
29-UUN-2001; 2001WO-US1785.
29-UUN-2001; 2001WO-US1785.
21-OCT-1997; 97US-063264P.
24-OCT-1997; 97US-063121P.
28-OCT-1997; 97US-063121P.
28-OCT-1997; 97US-063121P.
28-OCT-1997; 97US-063121P.
28-OCT-1997; 97US-06374P.
21-OCT-1997; 97US-06374P.
21-NOV-1997; 97US-06374P.
21-NOV-1997; 97US-06372P.
11-DEC-1997; 97US-064123P.
11-DEC-1997; 97US-064120P.
11-DEC-1997; 97US-06425P.
11-DEC-1997; 97US-06425P.
11-DEC-1997; 97US-06425P.
11-DEC-1997; 97US-06425P.
11-MAR-1998; 98US-077649P.
20-MAR-1998; 98US-077632P.
21-MAR-1998; 98US-077632P.
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9708 - 063544P

9708 - 063734P

9708 - 063731P

9708 - 064103P

9708 - 064103P

9708 - 06420P

9708 - 077649P

9808 - 077649P

9808 - 077649P

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9808 - 07864P

9808 - 07864P

9808 - 080337P

9808 - 081049P

9808 - 081049P

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9808 - 081049P
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98US-083229-
98US-083422P-
98US-083495P-
98US-083496P-
98US-083496P-
98US-083496P-
98US-083496P-
98US-084366P-
98US-084366P-
98US-084366P-
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9805 - 08558 P

9805 - 08560 P

9805 - 0860 P

9805 - 08660 P

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9805 - 0870 P
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08-APR-1998;
09-APR-1998;
11-APR-1998;
21-APR-1998;
22-APR-1998;
22-APR-1998;
22-APR-1998;
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31-MAR-1998;
31-MAR-1998;
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29-APR-1998;
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22-MAY-1998;
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          VTLALILLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 60
                                                                                                                                                                                                      VTLALLILAGLTALEANDPFANKDDFFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 60
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             secreted protein; transmembrane protein; antiatrhritic; osteopathic; adrenal tumour; lung tumour; breast tumour; prostate tumour; rectal tumour; our; liver tumour; TNR-alpha release; arthritis; sis factor alpha; chondrocyte cell; bone disorder;
cibody. Anti-PRO antibodies are useful in diagnostic PRO, by detecting its expression in specific cells, serum, and for affinity purification of PRO from cell culture or natural sources. ABU72109-ABU72192 he human PRO polypeptides of the invention.
                                                                                                                                                       0;
                                                                                                                    100.0%; Score 461; DB 24; Length 89; 100.0%; Pred. No. 1.2e-50; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                  ed/transmembrane protein, SEQ ID 200.
                                                                                                                                                                                                                                        KSSQKQHSPVPEKAIPLITPGSATTC 89
                                                                                                                                                                                                                                                          ndard; Protein; 89 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sorder, sports injury.
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COUNTY OF MANY

98WO-US21141. 98WO-US25108. 99WO-US05028.

2002US-0188767 98WO-US19330 99WO-US20111.

99WO-US12252

99WO-US10733

99WO-US28301 99WO-US31274. 2000WO-US00219.

99WO-US28551

2000WO-US08439. 2000WO-US13705. 2000WO-US14042.

2000WO-US14941

2000WO-US30952

2000WO-US05841. 2000WO-US06884.

2000WO-US05601.

2000WO-US04341. 2000WO-US04342. 2000WO-US04414. 2000WO-US05004.

98US-088033P 98US-088126P 98US-08812P 98US-08812P 98US-08812P 98US-08812P 98US-08811P 98US-08811P 98US-08811P 98US-08811P 98US-08812P 98US-08812P 98US-088812P 98US-088812P 98US-088812P 98US-088812P 98US-08885P 98US-08885P 98US-089538P 98US-08953P 98US-090525P 98US-090435P

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1 MERVILALLILAGLIALEANDPFANKDDPFXYDWKNLQLSGLICGGLLAIAGIAA
                                                                                                                                                                                                          Human; secreted protein; transmembrane protein; cytostatic; gene Therapy; TNF-Agonist-Alpha; chondrocyte stimulator; tumour; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour.
                                                                                                                                                       0
                                                                                                               Length 89;
                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human secreted and transmembrane protein PRO1069.
                                                                                                     100.0%; Score 461; DB 24;
100.0%; Pred. No. 1.2e-50;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                              CKYKSSQKQHSPVPEKAIPLITPGSATTC 89
                                                                                                                                                                                                                                                                                          CKYKSSQKQHSPVPEKAIPLITPGSATTC 89
                                                                                                                                                                                                                                                                                                                                                                                                     ABU66001 standard; Protein; 89
98US-098821P.
98US-098843P.
98US-099602P.
98US-099741P.
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99WO-US10538
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99WO-US20111.
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99WO-US28551.
99WO-US31274.
2000WO-US00219.
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2000WO-US32678.
2000WO-US34956.
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2000WO-US15264
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2000WO-US14042
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                                                                                                Query Match
Best Local Similarity 100.0
Matches 89, Conservative
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                     02-SEP-1998;
09-SEP-1998;
10-SEP-1998;
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08-MAX-1999;

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08-MAX-2000;

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98US-090696P 98US-090862P 98US-090863P 98US-091010P 98US-091359P 98US-091444P 98US-091486P 98US-091486P 98US-091486P 98US-091628P 98US-091632P 98US-091632P 98US-091632P 98US-091632P 98US-091632P 98US-091632P 98US-096012P 98US-096012P

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2001WO-1021/106.
2001WO-10221/09.
970US-002866.P.
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970US-002866.P.
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970US-002812.P.
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PR 05-JUN-1998 980S-08652F
PR 10-JUN-1998 980S-08652F
PR 110-JUN-1998 980S-08652F
PR 110-JUN-1998 980S-08652F
PR 110-JUN-1998 980S-08812F
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PR 22-JUN-1998 980S-09024F
PR 22-JUN-1998 980S-09024F
PR 22-JUN-1998 980S-09026F
PR 22-JUN-1998 980S-09066F
PR 22-JUN-1998 980S-0916F
PR 17-AUG-1998 980S-0916F
PR 26-AUG-1998 980S-0916F
PR 26-AUG-1998 980S-0919F
PR

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The invention discloses human nucleic acids encoding secreted and transmembrane (PRO) polypeptides. Also disclosed is an antibody to transmembrane (PRO) polypeptides. Also disclosed is an antibody to specifically binds to the PRO polypeptide, a method for stimulating release of tumour necrosis factor alpha (TNF-alpha) from human bloom actification of chondrocyte cells by contacting the blood a PRO polypeptide, a method for stimulating the presence tumour in a mammal and an oligonucleotide probe derived from any PRO nucleotide sequences. The nucleotide sequences are useful as in chromosome and gene mapping, in generating antisense RNA and D preparing PRO polypeptides by recombinant techniques and in gene or sequences are useful as a molecular weight markers for potabin electrophoresis purposes, chromosome identification, as chromosome markers, as therapeutic for stimulating the release of TNF-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes detecting the presence of a tumour. The PRO polypeptides and nucle acids may also be used diagnostically for tissue typing. The sequence of presented in ABU67406-ABU67710 are the PRO polypeptides of the in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New secreted and transmembrane PRO polypeptides and nucleic acids useful in gene therapy, in chromosome and gene mapping, as chromcmarkers, in tissue typing, and in chromosome identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MERVILALLILAGITALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAV
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Smith V, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Fig 200; 706pp; English.
                                                                                                                                                                        2000US-0644848.
2000US-0644610.
2000US-065350.
200US-0747259.
2001US-0816744.
2001US-0816744.
                                                                99US-0311832.
99US-0380137.
99US-0380138.
99US-0380142.
99US-0403297.
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2001US-0918585.
2001US-0924419.
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99US-0254311
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2001US-0874503
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N-PSDB; ACA05799.
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18-SEP-2000;
08-NOV-2000;
20-DEC-2000;
22-MAY-2001;
10-MAY-2001;
25-MAY-2001;
25-MAY-2001;
                                                                  14-MAY-1999;
14-MAY-1999;
25-AUG-1999;
25-AUG-1999;
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22-AUG-2000;
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                                                                                    TLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK
                                                                                                                                                                                                                                                                                                                                                                           and transmembrane protein; PRO; TNF-alpha; factor alpha; chondrocyte cell; tumour; gene therapy;
                                                              Gaps
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                             Score 461; DB 24; Length 89; Pred. No. 1.2e-50;
                                                           Indels
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                                                          0; Mismatches
                                                                                                                                                SSOKOHSPVPEKAIPLITPGSATTC 89
                                                                                                                                                                   SSQKQHSPVPEKAIPLITPGSATTC 89
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                             100.08;
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2001WO-US17800.
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Godowski PJ,

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9705-063734P

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9705-063131P

9705-064122P

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 29-OCT-1997;
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21-NOV-1997;
24-NOV-1997;
24-NOV-1997;
11-DEC-1997;
11-DEC-1997;
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31-MAR-1998;
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33-APR-1998;
34-APR-1998;
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37-APR-1998;
37-APR-1998;
37-APR-1998;
38-APR-1998;
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109 - UUN - 1998
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22-MAY-1998;
28-MAY-1998;
28-MAY-1998;
02-JUN-1998;
02-JUN-1998;
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  cytostatic; chromosome mapping; gene mapping; trophoresis; tumour necrosis factor-alpha; TNF-alpha; blood; differentiation; chondrocyte proliferation; tumour.
            KSSOKOHSPVPEKAIPLITPGSATTC
                          KSSOKOHSPVPEKAIPLITPGSATTC
                                                                                    ndard; Protein; 89 AA.
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98WO-US21141. 98WO-US25108. 99WO-US10733. 99WO-US1252. 99WO-US20111.

2002US-0173697

-A1.

lypeptide #100. (first entry)

99WO-US28301.

2000WO-US04341. 2000WO-US04414. 2000WO-US05004. 2000WO-US05601. 2000WO-US05611. 2000WO-US05841. 2000WO-US05841. 2000WO-US05841.

2000WO-US14042. 2000WO-US1234941. 2000WO-US13328. 2000WO-US13328. 2000WO-US13678. 2001WO-US14956. 2001WO-US14956. 2001WO-US14956. 2001WO-US1969. 2001WO-US1969. 2001WO-US1969. 2001WO-US1969. 2001WO-US1969. 2001WO-US1969. 2001WO-US1969. 97US-0531319. 97US-0531219. 97US-063121P. 97US-063121P. 97US-063121P. 97US-063121P. 97US-063121P.

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61 CKYKSSQKQHSPVPEKAIPLITPGSATTC 89
                                                                                                       Search completed: January 6, 2004, 16:02:53
Job time : 41 secs
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98US - 089105P - 98US - 089513P - 98US - 089513P - 98US - 089538P - 98US - 089538P - 98US - 089538P - 98US - 089553P - 98US - 089553P - 98US - 099552P - 98US - 090544P - 98US - 090548P - 98US - 090548P - 98US - 090548P - 98US - 09059P - 98US - 09099P - 98US - 0999P - 98US - 099P - 98US - 09
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1 MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAV.
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NUMBER OF SEQ ID NOS: 12
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
US-08-738-127-6
US-09-213-392-6
US-09-268-140-2
US-09-268-140-2
US-09-198-452A-112
US-09-690-454-16
US-09-328-352-7324
US-09-336-643A-4
US-09-336-643A-4
US-09-107-522A-3725
US-09-1107-522A-3725
US-09-1107-523A-3725
US-09-120-365-3
US-09-149-476-341
US-09-318-642-13
US-09-252-991A-28424
US-08-930-830B-5
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100.0%; Pred. No. 8.5e-52;
iive 0; Mismatches 0;
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Parent No. 6478825
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Bostsein, Javid
APPLICANT: Bostsein, Javid
APPLICANT: Bestrein, Javid
APPLICANT: Batsein, David
APPLICANT: Baton, Dan L.
                                                                                                                                                                                                                                                                                                                                               US-09-289-349-11
; Sequence 11, Application US/09289349
; Patent No. 6277574
; GENERAL INFORMATION:
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Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: 1900433CD1
US-09-289-349-11
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Gerber, Hanspeter
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   ORGANISM: Homo sapiens
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Best Local Similarity
Matches 89; Conserv
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US-09-996-243-262
 SEQ ID NO 11
LENGTH: 89
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APPLICANT:
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   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Appl Sequence 56, App Sequence 58, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 473, App
Sequence 199, App
Sequence 606, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 405, App
Sequence 424, App
Sequence 6, Appli
                                                                                           / Search time 22 Seconds
(without alignments)
171.167 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the number of results predicted by chance to have a than or equal to the score of the result being printed, id by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                 TERVTLALLLLAGLTALEAN........HSPVPEKAIPLITPGSATTC
                                                                                                                                                                                                                                                                                                                                                                                                                            /ogn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-289-349-11

US-09-996-243-262

US-08-724-88-127-5

US-08-725-531-5

US-09-213-392-5

US-09-213-392-4

US-08-213-392-4

US-09-213-392-4

US-09-213-392-4

US-09-213-392-4

US-09-213-392-4

US-09-213-392-4

US-09-213-392-1

US-09-149-476-606

US-08-223-405
                                                                                                                                                                                                                                                                                     s satisfying chosen parameters:
                                                                                                                                                                                                                                                        3717 segs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                        .nimum Match 0%
iximum Match 100%
.sting first 45 summaries
                                                                   in search, using sw model
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Length 89;

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PRIOR APPLICATION NUMBER: 60/08655
PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1998-06-09
PRIOR PELLING DATE: 1998-06-10
PRIOR PELLING DATE: 1998-06-10
PRIOR PELLING DATE: 1998-06-10
PRIOR PELLING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08826
PRIOR PELLING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08826
PRIOR FILING DATE: 1998-06-10
PRIOR PELLING DATE: 1998-06-11
PRIOR PELLING DATE: 1998-06-16
PRIOR PELLING DATE: 1998-06-17
PRIOR PELLING DATE: 1998-06-18
PRIOR PELLING DATE: 1998-06-22
PRIOR PELLING DATE: 1998-06-22
PRIOR PELLING DATE: 1998-06-22
PRIOR PELLING DATE: 1998-06-23
PRIOR PELLING DATE: 1998-06-24
PRIOR PELLING DATE: 19
                                                                                                                                                                                                                                                                                                                                        TION: Societed and Transmembrane Polypeptides and Nucleic TION: Acids Encoding the Same P2730P1C13
                                                                                                                                                                                                                                                                                                                                                                                                                 ATION NUMBER: US/09/996,243
DATE: 2001-11-14
ION NUMBER: 60/049787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATE: 1997-11-12
ION NUMBER: 60/065311
ATE: 1997-11-13
ION NUMBER: 60/066770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATE: 1998-06-05
ION NUMBER: 60/088212
ATE: 1998-06-05
ION NUMBER: 60/088217
ATE: 1998-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATE: 1998-06-04
ION NUMBER: 60/088030
ATE: 1998-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATE: 1997-06-16
ION NUMBER: 60/062250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATE: 1997-10-17
ION NUMBER: 60/065186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATE: 1998-02-25
ION NUMBER: 60/078910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATE: 1998-03-20
ION NUMBER: 60/083322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTE: 1998-05-07
ON NUMBER: 60/087106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TON NUMBER: 60/087759
ATE: 1998-06-02
TON NUMBER: 60/087827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATE: 1998-06-04
CON NUMBER: 60/088029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATE: 1998-06-04
ION NUMBER: 60/088326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 1998-06-04
| NUMBER: 60/088167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ON NUMBER: 60/088202
                                           lowski, Paul J.
imaldi, J. Christopher
                                                                                                                                                                                                                                          nas, Daniel
tanabe, Colin K.
lliams, P. Mickey
od, William I.
                                                                                                                                                                   oni, Nicholas F.

y, Margaret Ann

ewart, Timothy A.

nas, Daniel
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    rritsen, Mary E.
ldard, Audrey
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                                                                                    rney, Austin L.
javin, Ivar J.
                                                                                                                                  pier, Mary A.
                                                                                                                                                                                                                                                                                                                                 Zemin
                                                                                                                                                         ,James
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                                                                                                                                                                                                                                             1 MEBITCAFLLLLAGLPALEASDP-VDKDSPFYYDWBSLQLGGLIFGGLLCIAGIAN
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                                                                                                                                   DB 4; Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08725531
Patent No. 5756310
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Gold, Surya K.
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                 60.0%; Score 276.5; DB 4;
66.7%; Pred. No. 4.2e-28;
iive 8; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
55.6%; Score 256.5; DB 1;
Best Local Similarity 61.5%; Pred. No. 1.5e-25;
Matches 56; Conservative 11; Mismatches 17;
                                                                                                                                                                                                                                                                                                    60 KCKYKSSQKQHSPVPEKAIPLITPGSATIC 89
                                                                                                                                                                                                                                                                                                                                60 KCKCRRTHKP-SSLPGKATPLIIPGSANTC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FASTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: Filed Herewith
RRIOR APPLICATION NUMBER:
FILING APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF-0128 US
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ATTORNEY AGENT INFORMATION:
NAME: BILLING, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: FF-01
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-85-055
TELEPHONE: 415-85-055
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IEM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                 Query Match
Best Local Similarity 66.79
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 87 amino acids
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TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 Port
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si:
    ; SEQ ID NO 58
; LENGTH: 88
; TYPE: PRT
; ORCANISM: Mouse
US-09-724-864-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , CLONE: 9
US-08-725-531-5
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180n, James G.

10N: Polynucleotides, polypeptides expressed

100: by the polynucleotides and methods for their use.

11000.1050U1

TION NUMBER: US/09/724,864

DATE: 2000-11-28

ON NUMBER: US. No. 6380362 60/171,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 461; DB 4; Length 89; arity 100.0%; Pred. No. 8.5e-52; onservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSOKOHSPVPEKAIPLITPGSATTC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ for Windows Version 4.0
TE: 1998-06-24

NN NUMBER: 60/090535

TE: 1998-06-24

NN NUMBER: 60/090540

TE: 1998-06-24

NN NUMBER: 60/090557

TE: 1998-06-24

NN NUMBER: 60/09057

TE: 1998-06-25

NN NUMBER: 60/090694

TE: 1998-06-25

NN NUMBER: 60/090694

TE: 1998-06-25

NN NUMBER: 60/090694

TE: 1998-06-25

NN NUMBER: 60/090696

TE: 1998-06-25

NN NUMBER: 60/090696

TE: 1998-06-25

NN NUMBER: 60/090863

TE: 1998-06-25

NN NUMBER: 60/090863

TE: 1998-06-26

NN NUMBER: 60/091360

TE: 1998-06-26

NN NUMBER: 60/091360

TE: 1998-06-26

NN NUMBER: 60/091360

TE: 1998-06-26

NN NUMBER: 60/091544

TE: 1998-07-01

NN NUMBER: 60/091544

TE: 1998-07-01

NN NUMBER: 60/091544

TE: 1998-07-02

NN NUMBER: 60/091549

TE: 1998-07-02

NN NUMBER: 60/091978

TE: 1998-07-02

NN NUMBER: 60/091978

TE: 1998-07-02

NN NUMBER: 60/091978

TE: 1998-07-07

NN NUMBER: 60/091978
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1 MERVTLA-LLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLLCGGLLAIAGIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-083-661-5

Sequence 5, Application US/09083661

Patent No. 5955283

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 KCKYKSSQKQHSP~~VPEKAIPLITPGSATT 88
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER REDABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,661
                                                                                                                                                                                                      SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/213,392
                                                                                                                                                                                                                                                                   FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/083,661
                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPRENCE/DOCKET NUMBER: PF-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                          ZIP: 94304
COMPUTER REDABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIDIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 61.5*
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 87 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 951423
US-09-213-392-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid STRANDEDNESS: si
                                                           Palo Alto
                                                                          CA
T.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     u.s.
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                                                         CITY: Pa
STATE: CA
COUNTRY:
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITCAFLLVLAGLPVLEANGP-VDKGSPFYYDWESLQLGGMIFGGLLCIAGIAMALSG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bandman, Olga
Goli, Surya K.
ENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
QUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.6%; Score 256.5; DB 2; Length 87.
larity 61.5%; Pred. No. 1.5e-25;
Conservative 11; Mismatches 17; Indels
                                                                                                                                                                                       Bandman, olga
Hawkins, Phillip R.
ENTION: NOVEL HUMAN PHOSPHOLEMMAN HOMOLOG
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     YKSSOKOHSP--VPEKAIPLITPGSATT 88
                                                                                                                                                                                                                                                               ČE ADDRESS:
Incyte Pharmaceuticals, Inc.
174 Porter Drive
                           ---CRRNHTPSSLPEKVTPLITPGSAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF-0141 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYSTEM: DOS
FRACESQ Version 1.5
ICATION DATA:
N NUMBER: US/08/738,127
E: Filed Herewith
ATION DATA:
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                                                                                                                                   lication US/08738127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lings, Lucy J.
ON NUMBER: 36,749
DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATION INFORMATION:
415-855-0555
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R SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RACTERISTICS: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide
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                                                                                                                                                                                                                                                QUENCES:
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PF-0128 US

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1 MERVILALLL-LAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIA
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ທ
                                                                                                                                  DB 1; Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4. Application US/08725531
Patent No. 5756310
GENERAL INFORMATION:
APPLICANT: Bandam, Olga
APPLICANT: Goli, Surya K.
TITLE OF INFORMION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSES: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 46.5%; Score 214.5; DB 1; Length 87; Best Local Similarity 54.5%; Pred. No. 3.8e-20; Matches 48; Conservative 11; Mismatches 24; Indels
                                                                                                                                                                    24; Indels
                                                                                                                              Query Match

46.5%; Score 214.5; DB 1
Best Local Similarity 54.5%; Pred. No. 3.8e-20;
Matches 48; Conservative 11; Mismatches 24
                                                                                                                                                                                                                                                                               60 KCKYKSSQKQ-HSPVPEKAIPLITPGSA 86
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OURRATING SYGTEM: DOS
SOFTWARE: FASTESQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,531
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
TELEBORMUNICATION INPORMATION:
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TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CTONE: 1085026
     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diskette
                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                        ; TOPOLOGY: linear
US-08-289-247B-4
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         55.6%; Score 256.5; DB 2; Length 87; 61.5%; Pred. No. 1.5e-25; ive 11; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .eder, Philip
NTION: Detection and Treatment of Breast
NTION: Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSSQKQHSP--VPEKAIPLITPGSATT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --CRRNHTPSSLPEKVTPLITPGSAST 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1: 3.5" Diskette, 1.44 Mb IBM PS/2 Model 50Z or 55SX 3YSTEM: MS-DOS (Version 5.0) WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cer-Brady, Kristina
NN NUMBER: 39,109
OCKET NUMBER: 00383/021001
NTION INFORMATION:
                                                                                                                              PF-0128 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | NUMBER: US/08/289,247B |: August 11, 1994 | VION DATA:
3:
VIION DATA:
1 NUMBER: 08/725,531
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E ADDRESS:
Clark & Elbing LLP
                                                                                      ings, Lucy J.
N NUMBER: 36,749
NOCKET NUMBER: PF-0
VION INFORMATION:
415-855-0555
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                                                                                                                                                                               428-0200
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                                                                    IT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                         amino acids
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JRCE:
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1 MERVILALLI-LAGLIALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGI?
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US-09-083-661-4
; Sequence 4, Application US/09083661
; Sequence 4, Application US/09083661
; Patent No. 595283
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
46.5%; Score 214.5; DB 2; Length 87;
Best Local Similarity 54.5%; Pred. No. 3.8e-20;
Matches 48; Conservative 11; Mismatches 24; Indels
NUMBER OF SEQUENCES: 6
CORRESPONDENCE PORRESS:
ADDRESSEE: Incyce Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/083,661
FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION WHERE: 36,749
REFERENCE/DOCKET NUMBER: PF-0128 US
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 KCKCKFGQKSGHH--PGETPPLITPGSA 85
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                                                                                                                                                                                                 SOFTWARE: FASTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/213,392
FILING DATE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                          COUNTRY:

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MITTER: DISKETTE
MITTER: DISKETTE
MITTER: DISKETTE
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS: si
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CLONE: 1085026
                                                                          Palo Alto
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                                                                                            STATE: C. COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTLGLLVFLAGFPVLDAND-LEDKNSPFYYDWHSLQVGGLICAGVLCAMGIIIVMSA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Gaps
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ENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.5%; Score 214.5; DB 2; Length 87 larity 54.5%; Pred. No. 3.8e-20; Conservative 11; Mismatches 24; Indels
                                                                                                                                                                                                           Bandman, Olga
Hawkins, Phillip R.
ENTION: NOVEL HUMAN PHOSPHOLEMMAN HOMOLOG
                                                                                                                                                                                                                                                                                      CE ADDRESS:
Incyte Pharmaceuticals, Inc.
174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | | | | | | CKFGQKSGHH--PGETPPLITPGSA 85
                    YKSSQKQ-HSPVPEKAIPLITPGSA 86
                                                    CKFGOKSGHH--PGETPPLITPGSA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKSSOKO-HSPVPEKAIPLITPGSA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSTEM: DOS
FASTSEQ Version 1.5
ICATION DATA:
N NUMBER: US/08/738,127
E: Filed Herewith
ATION DATA:
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                                                                                                                                                     lication US/08738127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lings, Lucy J.
ON NUMBER: 36,749
DOCKET NUMBER: PF-0
ATION INFORMATION:
415-855-0555
415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acids
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RACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Diskette
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URCE:
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85026
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14 LTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKSSQK(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.0%; Score 129; DB 4; Length 92; Best Local Similarity 41.3%; Pred. No. 4e-09; Matches 26; Conservative 15; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 120, Application US/09247155A
Fatent No. 6312922
GENERAL INFORMATION:
APPLICANT: Dunas Milne Edwards, Jean-Baptiste
APPLICANT: Dunas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF NIVENTION: Complementary DNAS
FILE REFERENCE: GENSET: 021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT APPLICATION NUMBER: 60/074,121
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
FARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           % Sequence 3, Application US/08725531; Sequence 3, Application US/08725531; Patent No. 5756310; GENERAL INFORMATION:
APPLICANT: Bandman, Olga
      92 amino acids
                      TYPE: amino acid
STRANDENESS: single
TOPCLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
IMBERRY: PRESNOTOS
CLONE: 786812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Parent.pm
SEQ ID NO 120
LENGTH: 92
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: SIGNAL
; LOCATION: -20..-1
US-09-247-155-120
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73 PDE 75
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Incyte Pharmaceuticals, Inc.
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ALIGNMENTS

APPLICANT: Godowatt, Paul Y.
APPLICANT: Godowatt, Paul Y.
APPLICANT: Godowatt, Paul Y.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurmary, Austin L.
APPLICANT: Marier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLI :62, Application US/09989722 US20020072067A1 Fong, Sherman Gerber, Hanspeter Gerritsen, Mary E. Goddard, Audrey Desnoyers, Luc Eaton, Dan L. Ferrara, Napoleone : Ashkenazi, Avi J. : Baker, Kevin P. : Botstein, David FORMATION 2-262

Sequence 262, App Sequence 262, App

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Description

SUMMARIES

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wart, Timothy A.
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liams, P. Mickey
i, William I.
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avin, Ivar J.
ier, Mary A.
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ritsen, Mary E.
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enazi, Avi J. er, Kevin P. stein, David

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wart, 11... Daniel

James

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and NUTITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/091519
PRIOR PILING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
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; Patent No. US20020072496Al
; GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watenabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Ferrara, Napoleone
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Goddard, Audrey
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Napier, Mary A.
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Best Local Similarity
Matches 89; Conserve
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION UNMERS: 60/08569
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DR APPLICATION NUMBER: 60/088030

DR FILING DATE: 1998-06-04

DR APPLICATION NUMBER: 60/088326

DR FILING DATE: 1998-06-04

DR APPLICATION NUMBER: 60/088326

DR FILING DATE: 1998-06-04

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DR APPLICATION NUMBER: 60/088167
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R APPLICATION NUMBER: 60/088810
R FILING DATE: 1998-06-10
R APPLICATICN NUMBER: 60/088824
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R APPLICATICN NUMBER: 60/088826
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R APPLICATION NUMBER: 60/088858

R FILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/088861

R APPLICATION NUMBER: 60/088861

R APPLICATION NUMBER: 60/088876

R FILING DATE: 1998-06-11
                                   APPLICATION NUMBER: 60/083322
FILING DATE: 1986-04-28
PAPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026
FILING DATE: 1998-06-04
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FILING DATE: 1998-05-28
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APPLICATION NUMBER: 60/088212
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FILING DATE: 1998-06-09
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APPLICATION NUMBER: 60/088217
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088742
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FILING DATE: 1998-06-12
APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089538
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598
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FILING DATE: 1998-06-16
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TION: Secreted and Transmembrane Polypeptides and Nucleic
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100.0%; Pred. No. 5.8e-48;
iive 0; Mismatches 0;
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                                                                                       TION NUMBER: 60/091633

DATE: 1998-07-02

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DATE: 1998-07-09
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                    DATE: 1998-07-02
TION NUMBER: 60/091626
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ION NUMBER: 60/049787
ATE: 1997-06-16
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ATE: 1997-10-17
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ATE: 1997-11-13
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NUMBER: 60/078910
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ATE: 1997-11-24
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dowski, Paul J.
imaldi, J.Christopher
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tanabe, Colin K.
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od, William I.
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y, Margaret Ann
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mas, Daniel
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tton, Dan L.
rrara, Napoleone
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ırritsen, Mary E.
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iker, Kevin P.
itstein, David
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pier, Mary A.
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WIE: 1998-06-24

ON WUMBER: 60/09044

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WIE: 1998-06-25

ON WUMBER: 60/09054

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APPLICANT: Zhang, Zemin TILLE OF INVENTION: Secreted and Transmembrane Polypeptides and NucTILLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PLC70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DAIE: 2001-11-20
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100.0%; Pred. No. 5.8e-48;
live 0; Mismatches 0;
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
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PRIOR PELING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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Patent No. US20020103125A1
GENERAL INFORMATION:
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Watanabe, Colin K.
Williams, P. Mickey
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Botstein, David
Desnoyers, Luc
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DATE: 1998-06-11
ITON NUMBER: 60/08030

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PRIOR PELLING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR PELLING DATE: 1998-07-01
PRIOR PELLING DATE: 1998

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PRIOR FILING DATE: 1998-05-28

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PRIOR PLING DATE: 1998-06-03

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PRIOR PRIOR DATE: 1998-06-05

PRIOR PRILING DATE: 1998-06-10

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BR FILING DATE: 1998-06-12
BR PELLING DATE: 1998-06-16
BR PELLING DATE: 1998-06-16
BR APPLICATION NUMBER: 60/089512
BR APPLICATION NUMBER: 60/089514
BR PILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/089538
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APPLICATION NUMBER: 60/089598
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APPLICATION NUMBER: 60/089599
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APPLICATION NUMBER: 60/089600
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APPLICATION NUMBER: 60/089653
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1ION: Secreted and Transmembrane Polypeptides and Nucleic
1ION: Acids Encoding the Same
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100.0%; Pred. No. 5.8e-48;
tive 0; Mismatches 0;
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DATE: 2001-11-19
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ATE: 1998-07-07
ION NUMBER: 60/091982
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ION NUMBER: 60/092182
ATE: 1998-07-09
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ON NUMBER: 60/049787
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TE: 1997-10-17
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TE: 1997-11-12
ON NUMBER: 60/065311
TE: 1997-11-13
ON NUMBER: 60/06570
TE: 1997-11-24
ON NUMBER: 60/076945
TE: 1998-02-25
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avin,Ivar J.
ier,Mary A.
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anabe, Colin K.
liams, P. Mickey
d, William I.
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ritsen, Mary E.
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ni,Nicholas F.
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er, Kevin P.
stein, David
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ATE: 1998-06-18
TON NUMBER: 60/089947
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TON NUMBER: 60/08952
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TON NUMBER: 60/091360
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ION NUMBER: 60/091478
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ION NUMBER: 60/091982
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ATE: 1998-07-02
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ATE: 1998-07-02
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and N. TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2700FICLS
CURRENT APPLICATION NUMBER: US/09/991,073
CURRENT FILING DATE: 2001-11-14
PRIOR PELING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PILING DATE: 1997-11-12
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PRIOR PILING DATE: 1997-11-24
PRIOR PILING DATE: 1998-01-25
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Best Local Similarity 100.0%; Pred. No. 5.8e-48;
Matches 89; Conservative 0; Mismatches 0; Indels C
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Patent No. US20020127576A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Gurney,Austin L.
Kljavin,Ivar J.
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Watanabe, Colin K.
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Wood, William I.
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Roy, Margaret Ann
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Botstein, David
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R FILING DATE: 1990-06-24
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APPLICATION DATE: 1998-06-22
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PRIOR PILING DATE: 1998-06-11
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RAPELICATION NUMBER: 60/08033

RETLING DATE: 1998-06-04

RAPPLICATION NUMBER: 60/080326

RETLING DATE: 1998-06-05

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RAPPLICATION NUMBER: 60/080202

RAPPLICATION NUMBER: 60/080202

RAPPLICATION NUMBER: 60/080212

RETLING DATE: 1998-06-05

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RETLING DATE: 1998-06-07

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R APPLICATION NUMBER: 60/08940
R FILING DATE: 1998-66-16
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R FILING DATE: 1998-66-17
R APPLICATION NUMBER: 60/089518
R FILING DATE: 1998-66-17
R APPLICATION NUMBER: 60/08959
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TION: Secreted and Transmembrane Polypeptides and Nucleic
TION: Acids Encoding the Same
                                                                                       0; Gaps
                          100.0%; Score 461; DB 10; Length 89;
larity 100.0%; Pred. No. 5.8e-48;
Conservative 0; Mismatches 0; Indels
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DATE: 2001-11-14
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rney, Austin L.
javin, Ivar J.
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ATE: 1998-04-28
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n, James
oni, Nicholas F.
Y, Margaret Ann
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mas, Daniel
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Iliams, P. Mickey
od, William I.
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rrara, Napoleone
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuc
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLIJ
CURRENT APPLICATION NUMBER: US/09/991,163
                                                 1 MERVILALLLLAGLTALEANDPFANKDDPFYYDWKNLOLSGLICGGLLAIAGIAA
                                                                                            1 MERVILALLILAGLIALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAA
             0; Mismatches
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR PILING DATE: 1997-06.16
PRIOR APPLICATION NUMBER: 60/06220
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PRIOR PELING DATE: 1997-11-12
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PRIOR PAPLICATION NUMBER: 60/066770
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PRIOR PAPLICATION NUMBER: 60/075945
PRIOR PELING DATE: 1997-11-24
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PRIOR PILING DATE: 1998-04-28
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PRIOR PELING DATE: 1998-05-07
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Patent No. US20020132253A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/087106
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
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APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/087827
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Grimaldi, J.Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
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Napier, Mary A.
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Eaton, Dan L.
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Length 89;

Score 461; DB 10; Pred. No. 5.8e-48;

100.0%; 100.0%;

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Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e-48;
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ATE: 1998-06-19

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and NuTITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C22
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CURRENT PELING DATE: 2001-11-4
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                        61 CKYKSSQKQHSPVPEKAIPLITPGSATTC 89
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ION NUMBER:
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CON NUMBERS: 60/088028

CON NUMBERS: 60/088029

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| PRIOR APPLICATION NUMBER: 66/090254
| PRIOR PLILAND DATE: 1999-66-29
| PRIOR PLILAND DATE: 1999-66-20
| PRIOR APPLICATION NUMBER: 66/090355
| PRIOR PLILAND DATE: 1999-66-20
| PRIOR PLILAND DATE: 1999-66-24
| PRIOR PLILAND DATE: 1999-66-25
| PRIOR PLILAND DATE: 1999-60-00-01
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R APPLICATION NUMBER: 60/088030
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088033
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088326
R APPLICATION NUMBER: 60/088326
R FILING DATE: 1998-06-05
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R APPLICATION NUMBER: 60/088734

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R APPLICATION NUMBER: 60/088738

R APPLICATION NUMBER: 60/088742

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R APPLICATION NUMBER: 60/088888

R FILING DATE: 1998-06-11
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R FILING DATE: 1998-06-16

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R APELICATION NUMBER: 60/089514

R APELICATION NUMBER: 60/089532

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R APPLICATION NUMBER: 60/089501

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APPLICATION WUMBER: 60/088217
ELING DATE: 1998-06-05
APPLICATION NUMBER: 60/088655
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FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/089952
LILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090252
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
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TION: Secreted and Transmembrane Polypeptides and Nucleic
TION: Acids Encoding the Same
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DATE: 2001-11-19
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TON NUMBER: 60/065186
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TON NUMBER: 60/065311
ATE: 1997-11-24
TON NUMBER: 60/06770
ATE: 1997-11-24
TON NUMBER: 60/078910
ATE: 1998-02-25
TON NUMBER: 60/078910
ATE: 1998-04-28
TON NUMBER: 60/081106
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TON NUMBER: 60/081106
ATE: 1998-04-28
TON NUMBER: 60/087106
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ATE: 1998-06-04
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ION NUMBER: 60/049787
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TON NUMBER: 60/062250
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ION NUMBER: 60/087759
ATE: 1998-06
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ATE: 1998-06-02
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ATE: 1998-06-03
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ION NUMBER: 60/088025
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imaldi, J.Christopher
urney, Austin L.
javin, Ivar J.
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tanabe, Colin K.
lliams, P. Mickey
od, William I.
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oni,Nicholas F.
y, Margaret Ann
ewart, Timothy A.
umas, Daniel
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rrara, Napoleone
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iker, Kevin P.
itstein, David
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: 1998-06-23 NUMBER: 60/090429 : 1998-06-24 : 1998-06-23 NUMBER: 60/090355

ON NUMBER: 60/090431 ATE: 1998-06-24 CON NUMBER: 60/090435

NUMBER: 60/090444 : 1998-06-24 TE: 1998-06-24 ON NUMBER: 60/090445

1998-06-24

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nur
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC20
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CURRENT FILING DATE: 2011-114
PRIOR PELING DATE: 2011-114
PRIOR PELING DATE: 1997-06-16
PRIOR PILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-10-17
PRIOR PLING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PLING DATE: 1997-11-12
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065312
PRIOR PILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-20
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PRIOR PILING DATE: 1998-05-07
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PRIOR PILING DATE: 1998-05-07
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PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-08
PRIOR FILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
                  Sequence 262, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                              Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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Gerber, Hanspeter
Gerritsen, Mary E.
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Botstein, David
Desnoyers, Luc
Eaton, Dan I.
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US-09-992-598-262
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VIE. 1998-06-24

ON NUMBER: 60/090472

VIE: 1998-06-24

ON NUMBER: 60/090535

VIE: 1998-06-24

ON NUMBER: 60/090540

VIE: 1998-06-24

ON NUMBER: 60/09057

VIE: 1998-06-24

ON NUMBER: 60/09057

VIE: 1998-06-25

ON NUMBER: 60/090696

VIE: 1998-06-25

ON NUMBER: 60/090862

VIE: 1998-06-25

ON NUMBER: 60/090863

VIE: 1998-06-26

ON NUMBER: 60/091360

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ON NUMBER: 60/091360

VIE: 1998-07-01

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TE: 1998-07-01
ON NUMBER: 60/091519
TE: 1998-07-02
ON NUMBER: 60/091626
TE: 1998-07-02
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ON NUMBER: 60/091978
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ON NUMBER: 60/091962
TE: 1998-07-07
ON NUMBER: 60/091962
TE: 1998-07-07
ON NUMBER: 60/09187

ON NUMBER: 60/091544 TE: 1998-07-01

1 MERVTLALLLLAGITALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAA Length 89; ch 100.0%; Score 461; DB 10; Length E | Similarity 100.0%; Pred. No. 5.8e-48; 89; Conservative 0; Mismatches 0; Indels THING DATE: 1399-0-0-23

TRAPLICATION NUMBER: 60/090429

TREING DATE: 1998-06-24

TREING DATE: 1998-06-25

TREING DATE: 1998-06-26

TREING DATE: 1 R APPLICATION NUMBER: 60/091978
R FILING DATE: 1998-07-07
R APPLICATION NUMBER: 60/091982
R FILING DATE: 1998-07-07
R APPLICATION NUMBER: 60/092182
R FILING DATE: 1998-07-09 FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091544
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091626 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091633 FILING DATE: 1998-07-02 Best Local Similarity Matches 89; Conserv Query Match

RESULT 14 2.09-989-293A-262 ; Sequence 262, Application US/09989293A ; Patent No. US20020177164A1

ION NUMBER: 60/090254 ATE: 1998-06-22 ION NUMBER: 60/090349 ATE: 1998-06-23

TON NUMBER: 60/090355

ATE: 1998-06-22 ION NUMBER: 60/090252 ATE: 1998-06 ION NUMBER: 60/090246 ATE: 1998-06-22

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PRIOR FILING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-05
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PRIOR PILING DATE: 1998-06-09
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PRIOR APPLICATION NUMBER: 60/08868
PRIOR PILING DATE: 1998-06-11
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PRIOR FILING DATE: 1998-06-12
PRIOR PRINCATION NUMBER: 60/089105
PRIOR APPLICATION NUMBER: 60/089512
PRIOR PELING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089513
PRIOR APPLICATION NUMBER: 60/089514
PRIOR PELING DATE: 1998-06-17
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APPLICATION NUMBER: 60/090429
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FILING DATE: 1998-06-22
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FILING DATE: 1998-06-22
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TON: Secreted and Transmembrane Polypeptides and Nucleic
TON: Acids Encoding the Same
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TE: 1997-11-12
TE: 1997-11-13
ON NUMBER: 60/065311
TE: 1997-11-13
ON NUMBER: 60/06570
TE: 1998-02-25
ON NUMBER: 60/083122
TE: 1998-03-20
ON NUMBER: 60/083122
TE: 1998-05-28
ON NUMBER: 60/08759
ON NUMBER: 60/087609
TE: 1998-06-02
ON NUMBER: 60/08025
TE: 1998-06-02
ON NUMBER: 60/08025
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TE: 1998-06-04
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ON NUMBER: 60/049787
TE: 1997-06-16
ON NUMBER: 60/062250
TE: 1997-10-17
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ON NUMBER: 60/088033
TE: 1998-06-04
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.maldi, J. Christopher
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wart, Timothy A.
uas, Daniel
anabe, Colin K.
liams, P. Mickey
od, William I.
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Tritsen, Mary E.
Idard, Audrey
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avin, Ivar J.
Jer, Mary A.
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                          cenazi, Avi J.
cer, Kevin P.
stein, David
snoyers, Luc
con, Dan L.
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ION NUMBER: 60/090535 ATE: 1998-06-24 ION NUMBER: 60/090540 ATE: 1998-06-24 ION NUMBER: 60/090542 ATE: 1998-06-24

JMBEA. 1998-06-24 "WRER: 60/090472

ION NUMBER:

ATE: 1998-06-24 TON NUMBER: 60/090445

ION NUMBER: 60/090444 ATE: 1998-06-24

1998-06-24

ATE: 1998-06-24 ION NUMBER: 60/090435

ION NUMBER: 60/090431

TON NUMBER: 60/090678 ATE: 1998-06-25 TON NUMBER: 60/090690 ATE: 1998-06-25

ATE: 1998-06-24 TON NUMBER: 60/090676

ION NUMBER: 60/090557 ATE: 1998-06-24

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ATE: 1998-06-25 ION NUMBER: 60/090694 ATE: 1998-06-25 ION NUMBER: 60/090695

ATE: 1998-06-25 ION NUMBER: 60/090696 ATE: 1998-06-25 ION NUMBER: 60/090862 ATE: 1998-06-26

ATE: 1998-06-26 ION NUMBER: 60/090863 ATE: 1998-06-26 ION NUMBER: 60/091360 ATE: 1998-07-01

ATE: 1998-07-02 ION NUMBER: 60/091544 ATE: 1998-07-01 ATE: 1998-07-01 ION NUMBER: 60/091519 ATE: 1998-07-02

ON NUMBER: 60/091478

ATE: 1998-07-02 ION NUMBER: 60/091626 ATE: 1998-07-02 ATE: 1998-07-02 ION NUMBER: 60/091633 ATE: 1998-07-02 ION NUMBER: 60/091978 ATE: 1998-07-07

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THILE OF INVENTION: Secreted and Transmembrane Polypeptides and NY TITLE OF INVENTION: Acids Encoding the Same FILE REPERRACE, P2730PLG4.

THILE OF INVENTION: Acids Encoding the Same FILE REPERRACE, P2730PLG4.

CURRENT APPLICATION WINDER: 60/049787

PRIOR PRIOR OF FILING DATE: 1997-60-162

PRIOR FILING DATE: 1997-60-162

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PRIOR PELING NUMBER: 60/065166

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PRIOR PELING DATE: 1998-10-23

PRIOR PELING DATE: 1998-10-23

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PRIOR PELING DATE: 1998-10-30

PRIOR PELING DAT
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Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
Zhang, Zemin
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Paoni, Nicholas F.
Roy, Margaret Ann
   Ferrara, Napoleone
                                                           Gerber, Hanspeter
Gerritsen, Mary E.
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Kljavin, Ivar J.
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KSSOKOHSPVPEKAIPLITPGSATTC 89

100.0%; Score 461, DB 10; Length 89; 100.0%; Pred. No. 5.8e-48; Live 0; Mismatches 0; Indels

Conservative

ATE: 1998-07-07 ION NUMBER: 60/092182

TE: 1998-07-09

NUMBER: 60/091982

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ON NUMBER: 60/088202
ON NUMBER: 60/088212
ON NUMBER: 60/088217
TE: 1998-06-05
ON NUMBER: 60/08855
TE: 1998-06-10
ON NUMBER: 60/08834
TE: 1998-06-10
ON NUMBER: 60/08834
TE: 1998-06-10
ON NUMBER: 60/08834
TE: 1998-06-10
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TE: 1998-06-11
ON NUMBER: 60/08959
TE: 1998-06-17
ON NUMBER: 60/08959
TE: 1998-06-19
ON NUMBER: 60/08958
TE: 1998-06-19
ON NUMBER: 60/08958
TE: 1998-06-2
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100.0%; Score 461, DB 10;
Best Local Similarity 100.0%; Pred. No. 5.8e-48;
Matches 89; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/090449
PRIOR FILING DATE: 1938-06-24
PRIOR FILING DATE: 1938-06-24
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PRIOR PILING DATE: 1938-06-24
PRIOR FILING DATE: 1938-06-24
PRIOR PAPLICATION NUMBER: 60/090535
PRIOR PAPLICATION NUMBER: 60/090535
PRIOR PAPLICATION NUMBER: 60/090540
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PRIOR PLING DATE: 1998-06-24
PRIOR PAPLICATION NUMBER: 60/090570
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091544
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-07
                                     DR FILING DATE: 1998-06-24

DR APPLICATION NUMBER: 60/090445

PR FILING DATE: 1998-06-24

DR APPLICATION NUMBER: 60/090472

PR FILING DATE: 1998-06-24

DR APPLICATION NUMBER: 60/090535

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Search completed: January 6, 2004, 16:09:44 Job time : 32 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compu	in search, using sw model	nuary 6, 2004, 16:01:30 ; (w	-10-063-557-50 1 MERUTLALLLAGLTALEAN)SUM62 pop 10.0 , Gapext 0.5	3308 seqs, 96168682 residues	:s satisfying chosen parameters:	<pre>sth: 0 sth: 2000000000</pre>	inimum Match 0% aximum Match 100% isting first 45 summaries	IR 76:* pir1:* pir2:*

the number of results predicted by chance to have a than or equal to the score of the result being printed, ad by analysis of the total score distribution.

SUMMARIES

3. 31

Description	transmembrane arct		ינטייט	1		Na+/K+-exchanging	Na+/K+-exchanging	Na+/K+-exchanging	plastoquinol-plast	conserved hypothet	probable membrane		>		potassium channel	- w		probable transport		potassium channel	2	delayed rectifier	hypothetical prote	hypothetical prote	tion	potassium channel	Shaw type potaggin	1
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ggdef fami: uracil trai pyocin AP4: iron-stress: flagellum-s virulence 7 bodx perme hypothetice conserved 1 major histe O antigen 1 damage-ind probable DA O antigen 1 probable DA O antigen 1	TS. 1-1996 #text_change 05-Nov Y, H. 1995 Ssing an 'IsK-like' K+ cha MID:7597086 BL/DDBJ PIDN:AAA74691.1; PID:99514	DB 2; Length 87; 8-21; s 17; Indels 7; G YDWKNLOLSGLIGGGLIAIAGIAA YDWESLQLGGMIFGGLLCIAGIAM 88	tumors that share genetic IID:7970700 ; PIDN:CAA63606.1; PID:gl(status predicted <mat> ; DB 2; Length 88;</mat>
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62 13 62 13 62 13 62 13 62 13 62 13 62 13 62 13 62 15 13 62 15 13 62 15 15 15 15 15 15 15 15 15 15 15 15 15	RESULT 1 Lransmembrane protein - C'Species: Rattus norve C'Accession: 159391 R'Attali, B.; Latter, F Proc. Natl. Acad. Sci. A;Tile: A corticosterc A;Reference number: 159391 A;Acteus: preliminary; A;Acteus: preliminary; A;Acteus: preliminary; A;Acteus: preliminary; A;Acteus: preliminary; A;Acteus: preliminary; A;Acteus: 189391 A;Coss-references: GB:C;Genetics: A;Genetics: A;Genetics: A;Genetics:	MERVII MERVII MERVII MERVII	
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A; Molecule type: mRNA
A; Residues: 6-19, F', 21-53 ABW>
A; Residues: 6-19, F', 21-53 ABW>
A; Collins, J.H.; Leszyk, J.
B; Collins, J. Sefes-8668, 1987
A; Title: The "gamma-subunit" of Na, K-ATPase: a small, amphiphilic pro
A; Title: The "gamma-subunit" of Na, K-ATPase: a small, amphiphilic pro
A; Reference number: A27383; MUID:88163544; PMID:2831947
A; Noclecule type: protein
A; Noclecule type: protein
A; Residues: 1-19, F', 21-33 < CoL>
C; Complex: heterotrimer; alpha, beta, and gamma chain
C; Keywords: heterotrimer; hydrolase; transmembrane protein
        Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - bovine C; Species: Bos primigenius taurus (cattle) C;Date: 31-96-1993 #sequence_revision 03-Feb-1994 #text_change 19-A; C;Date: 31-96-1993 #sequence_revision 03-Feb-1994 #text_change 19-A; C;Accession: D46435; S315.25 R;Mercer, R.W.; Biemesderfer, D.; Bliss Jr., D.P.; Collins, J.H.; For J. Cell Biol. 121, 579-586, 1993 A;Title: Molecular cloning and immunological characterization of the A;Reference number: A46435; MuID:93252993; PMID:8387529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - sheep (fragment)
NyAlternate names: sodium pump gamma chain; sodium/potassium-depender
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 22-Nov-1993 #sequence revision 05-Dec-1998 #text_change 19-Ag
C;Accession: A46435; S31524; A27383
R;Mercer, R; B; B; B; B; B; B; B; B; C; D; Collins, J; F; For
J; Cell Biol: 121, 579-586, 1993
A;Title: Molecular cloning and immunological characterization of the
A;Reference number: A46435; MUID:93252993; PMID:8387529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: kidney
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:131232, NCBIP:12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Status: preliminary
A;Molecule type: mRNA
A,Rosidues: 1-58 AMBR>
A;Cross-references: EMBL:X70059; NID:g396; PIDN:CAA49663.1; PID:g397
A;Note: the authors translated the codon TTC for residue 25 as Pro
C;Keywords: hydrolase; transmembrane protein
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B46435
Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - rat
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Matches 18; Conserv
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A;Molecule type: mRNA
A;Residues: 6-53 <MER>
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tion and complete sequence determination of the major plasma membrane
r: A40533; MUID:91250422; PMID:1710217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               '0, 2176-2182, 1995 ... inovel phospholemman-like protein expressed in human breast tumors, ir. A55571; MVID:95138184; PMID:7836447
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                                                                                                                VTLALLL-LAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                   95 #sequence_revision 23-Mar-1995 #text_change 28-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                otein kinase major membrane substrate precursor - dog
lupus familiaris (dog)
92 #sequence_revision 28-Feb-1992 #text_change 05-May-1993
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.5%; Score 214.5; DB 2; Length 87; 54.5%; Pred. No. 1.3e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 92;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
  Pred. No. 1.3e-19;
; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.4%; Score 126.5; DB :41.4%; Pred. No. 7.3e-07 :1ve 15; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Mismatches
                                                                                                                                                                                                                              (CKFRQKP-SHRPGEGPPLITPGSAHNC 88
                                                                                                                                                                                         CYKSSOKOHSPVPEKAIPLITPGSATTC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YKSSOKO-HSPVPEKAIPLITPGSA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CKFGQKSGHH--PGETPPLITPGSA 85
                                                                                                                                                                                                                                                                                                                                                                                   nce inducer Mat-8 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cott, B.T.; Jones, L.R.
                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane protein
57.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 larity 54.5%
Conservative
                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB: M63934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSPVPEK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTGEPDE 75
                                                                                                                                                                                                                                                                                                                                                                                                             apiens
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C'Accession: F6988

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; J. C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret Nature 390, 249-256, 1997

A,Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, X.; Fuma, S.; C.; Fuller, M.; Halbert, M.; Holsappel, S.; Hosor Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapic A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Y., M.; Ogawa, K.; Ogiwara, A.; Odega, B.; Park, S.H.; Parro, V.; Pohl Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadiale, Y.; A,Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekguchi, J.; Sakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tos J.; Winters, P.; Tognoni, A.; Ta A;Title: The complete genome sequence of the Gram-positive bacterium E. A; Farerence numbers and MID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable membrane protein YPO3057 [imported] - Yersinia pestis (strain C,Species: Yersinia pestis
                                                                                       A;Residues: 1-160 <KAN>
A;Cross-references: EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAA1
A;Note: the nucleotide sequence was submitted to the EMBL Data Librar:
C;Genetics:
                                                                                                                                                                                                      A;Gene: petD
C;Superfamily: plastoquinol-plastocyanin reductase 17K protein; plast
C;Keywords: oxidoreductase; photosynthesis; thylakoid
F;24-144/Domain: plastoquinol-plastocyanin reductase 17K protein homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein ytcJ - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-529 <KUN>
A;Cross-references: GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 ALLLLAGLTAL-----EANDPFANKDD--PFYYDWKNLQLSGLICGGLLAIAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 ALDLOPHFVASDFPWVIDRLGKDRMKTAFAWKTLISKGILCAGGSDAPIEPVDPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                      Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 529;
                                                                                                                                                                                                                                                                                                                                                                                                          21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----MKNTÖTSGTICGG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           440 -SAVLR-----KSSHEQNGPSYNESECLPVYEAIKLYTEGSA
                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.4%; Score 71; DB 2 30.4%; Pred. No. 6.2; tive 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             Pred No. 1.4;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                   Score 72;
                                                                                                                                                                                                                                                                                                                                                   15.6%;
37.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 ALEANDPFANKDDPFYYD-
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 37.7%
Matches 23, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                   A, Status: preliminary
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
              A; Accession: S76298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 G 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 G 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: ytcJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
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                                                                                                                                      cloning and immunological characterization of the gamma polypeptide, A46415; MUID:93252993; PMID:8387529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocyanin reductase (EC 1.10.99.1) 17K protein - Synechocystis sp. (stracytochrome b6-f complex chain IV; plastoquinol-plastocyanin reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cloning and immunological characterization of the gamma polypeptide, A46435; MUID:93252993; PMID:8387529
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                                                    5; S31523 - emesderfer, D.; Bliss Jr., D.P.; Collins, J.H.; Forbush III, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            emesderfer, D.; Bliss Jr., D.P.; Collins, J.H.; Forbush III, B. 579-586, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                          #sequence_revision 03-Feb-1994 #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #sequence_revision 03-Feb-1994 #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 #sequence revision 10-Sep-1999 #text_change 03-Jun-2002
8; S76298; $15474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                          PIDN:CAA49666.1; PID:g56300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL:X70060, NID:951111; PIDN:CAA49664.1; PID:951112 translated the codon TTC for residue 25 as Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : EMBL:X58522; NID:g47376; PIDN:CAA41412.1; PID:g47377
                                                                                                                                                                                                                                                                                                       EMBL:X70062; NID:956299; PIDN:CAA49666.1; PID:
translated the codon TTC for residue 25 as Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKSSQKQHSPVPE 75
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.9%; Score 73.5; DB 32.7%; Pred. No. 0.33; ive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      16.4%; Score 75.5; DB
34.7%; Pred. No. 0.2;
ive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                              ase; transmembrane protein
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norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   arity 34.7 onservative
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                                                                                                      579-586,
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chorismate synthase [imported] - Chlamydophila pneumoniae (strain J13 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Ma
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A,Molecule type: DNA
A,Residues: 1-359 <STO>
A,Cross-references: GB:BA000008; NID:g8979410; PIDN:BAA99244.1; GSPDE
A,Experimental source: strain J138
C,Genetics:
                                                                                                                                                                  A)Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.;
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McC.
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                    A,Accession: D81536
A,Status: preliminary
A,Molecule type: DD8
A,Residues: 1.359 - REA>
A,Residues: 1.359 - REA>
A,Cross-references: GB:AE002240; GB:AE002161; NID:g7189720; PIDN:AAF:
A,Experimental source: strain AR39, HL cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: B86620
R,Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi
Nucleic Acids Res. 28, 2311-2314, 2000
A,Title: Comparison of whole genome sequences of chlamydia pneumoniae
A,Reference number: A86491; MUID:20330349; PMID:10871362
                                                       A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-359 <ARN>
A,Cross-references: GB:AE001684; GB:AE001363; NID:g4377366; PIDN:AAD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             potassium channel KCNA3 - human
N;Alternate names: potassium channel HLK3; potassium channel PCN3; sh
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 ALMSIPAAKGFEIGKGFASAQMRGSQYTDPFVMEGENITLKSNNCGGTLGGITIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 ALLLLAGLTALEANDPFANKD------DPFYYDWKNLQLSGLICGGLLAIAGIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 ALLLLAGLTALEANDPFANKD-----DPFYYDWKNLQLSGLIGGGLLAIAGIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 ALMSIPAAKGFEIGKGFASAQMRGSQYTDPFVMEGENITLKSNNCGGTLGGITIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 RIAFKPTSSIKRPCATVTKTKKETTYRTPQTGRHDPCVAIRAVPVV 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 RIAPKPTŚIKRPCATVTKTKKETTYRTPQTGRHDPCVAIRAVPVV 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.4%; Score 66.5; DB 2; Length 35:
23.6%; Pred. No. 13;
.ive 14; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----QHSP-VPEKAIPLI 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --QHSP-VPEKAIPLI
  A;Reference number: A72000; MUID:99206606; PMID:10192388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.4%; Score 66.5; Di 23.6%; Pred. No. 13; iive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 KCKYK--SSQK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: chorismate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: aroC
C;Superfamily: chorismate synthase
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Matches 25; Conservative
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tes 25; Conserv
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                                  A; Accession: A72004
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A38101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                              Iren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. I.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; d. K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, 327, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e and organization of Marchantia polymorpha chloroplast genome. II. Ger
r: S01567; MUID:89068686; PMID:2974085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s: EMBL:X04465; NID:g11640; PIDN:CAA28060.1; PID:g453590
uzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shi
74, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            se CP0815 [imported] - Chlamydophila pneumoniae (strains CWL029 and AR3 dophila pneumoniae, Chlamydia pneumoniae) 9 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene organization deduced from complete sequence of liverwort March
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ive genomes of Clamydia pneumoniae and C. trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z.; Fukuzawa, H.; Kohchi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
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                                                                                                                                                                                                                                                                                                                        s: GB:AL590842; PIDN:CAC92299.1; PID:g15981010; GSPDB:GN00175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGI-AAVLSGKCK 62
#sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plast Marchantia polymorpha
87 #sequence_revision 05-Jun-1987 #text_change 08-Oct-1999
                                                                                                                                                            equence of Yersinia pestis, the causative agent of plague.
et: AB0001, MUID:21470413, PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 okuchi, H.; Shiki, Y.; Takeuchi, M.; Chang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ation; gene organization, sites, features
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30.2%; Pred. No. 2.8;
ive 14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQKQHSPVPEKAIPLITPGSATT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEVLHSFVQWKSILAIVVGVAVS 98
                                                                                                                                                                                                                                                                                                                                                                                                            pothetical protein ytwI
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GB.M85217; NID:g186664; PIDN:AAA59457.1; PID:g186665
Hice, R.E.; Schaefer, K.; LaMendola, J.; Bell, G.I.; Nelson, D.J.; St
Sci. U.S.A. 88, 53-57, 1991
and functional expression in Xenopus oocytes of a human insulinoma and
s. A38556; MUID:91095456; PMID:1986382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-1p13.3
assium channel protein drkl
rotein; phosphoprotein; potassium channel; transmembrane protein; volt
4 #sequence_revision 07-Apr-1994 #text_change 01-Dec-2000
1; B38556; I52990
1; G : Hondy E : Schmid-Alliana, A : Mattei, M.G : Lesage, F : Ricar
y 8650-8657, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ne, P.B.; North, R.A.; Dooley, D.C.; Douglass, J.
163-172, 199.
ization and functional expression of genomic DNA encoding the human ly
IS2990; MUID:92189730; PMID:1547020
                                                                                                    , 8650-8657, 1992
functional expression, and regulation of two K(+) channels in human T
: A38101; MUID:92235098; PMID:1373731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , 21-36, 'V', 38-60,'L', 62-90,'V', 92-337,'S',339-418,'S',420-457,'LS',<
GB:MS5515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L', 62-523 <RES>
: GB:M38217; NID:g186670; PIDN:AAB88073.1; PID:g186671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SGKCKYKSSQKQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.4%; Score 66.5; DB 2; Length 52
20.1%; Pred. No. 19;
tive 14; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ary; translated from GB/EMBL/DDBJ
NA
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January 6, 2004, 16:04:40

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34 63.5 35 63.5 36 63.5 37 62.5	99	61 63	9 9			SUL Y4		DT 15-SEP-2003 DT 15-SEP-2003 DT 15-SEP-2003			RN [1] RP SEQUENCE FRC RA Strausberg FR RL Submitted (J			Geno	CC -!- SIMILARI	CC This SWISS-F	the Europ	use by modified	CC entities req CC or send an e	EMBL; P	DR Genew; HGNC:	Transmembra SIGNAL				SQ SEQUENCE 8	Query Match Best Local Simi	Matches 87;	Qy 1 MER	Db 1 MER	Oy 61 CKY
).1.6 Jompugen Ltd.		h time 11 Seconds t alignments) Million cell updates/sec		.HSPVPEKAIPLITPGSATTC 89			127863				by chance to have a the result being printed, e distribution.		no i thi trong of		Q63113 rattus norv Q61835 mus musculu		homo		ratt	mus m rattu		ovis	rattu		rati	rattus mus mu	P58550 homo sapien P27589 synechocyst	013001 xenopus lae P97808 mus musculu		092601 Chlamydia p	rattı
GenCore version 5.1.6 lopyright (c) 1993 - 2004 Compu	n search, using sw model.	<pre>uary 6, 2004, 16:00:10 ; Search (without 380.489 M</pre>	10-063-557-50	ERVTLALLLAGLTALEANHS)SUM62 >op 10.0 , Gapext 0.5	.863 segs, 47026705 residues	s satisfying chosen parameters:	rth: 0 rth: 2000000000	nimum Match 0% .ximum Match 100% .sting first 45 summaries	/issProt_41:*	the number of results predicted by than or equal to the score of the 'd by analysis of the total score d	SUMMARIES	ry ch Lenath DR In	 88 1 FXY4	887 88	88 1 FXY3 88 1 FXY3	92	92 1 PLM	94 1 FXY6	92 1 PLM	58 1 ATNG	53 1 ATNG 178 1 FXYS	178 1	80 1 FXY7	908	66 1 ATNG 70 1 ATNG	3.4 93 1 FXY8 HUMAN 3.6 160 1 PETD_SYNY3	61 184	135 1 YC66	359 1 AROC	525 1 CIK3

101 427

\$2 (1.8) (6) (0.13)(0.13)

homo											
P48547	P15388	P25122	P33690	063959	Q9jw39	69zhc9	010279	055274	001837	P22462	09pny0
KNC1_HUMAN	KNC1 MOUSE	KNC1_RAT	COMO BACSU	KNC3 MOUSE	SYL NEIMA	SILA SALTY	FUR4 SCHPO	ISIA SYNY3	P60 LISIV	KNC2 RAT	PURL_CAMJE
Н.	н,	Н	Н	H	Н	Н	-	Н	н	Н	Н
511	511	282	299	769	910	1048	581	342	524	638	728
13.8	13.8	13.8	13.6	13.6	13.6	13.6	13.4	13.3	13.3	13.1	13.1
63.5	63.5	63.5	62.5	62.5	62.5	62.5	62	61.5	61.5	60.5	60.5
34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

STANDARD;

(Mouse)

AR-2001)

M N.A.

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STRAIN-Wistar, TISSUB-Colon,
MEDLINE=95320221; PubMed=7597086;
Attali B., Latter H., Rachamim N., Garty H.,
"A corticosteroid-induced gene expressing an 'IsK-like' K+ chant activity in Xenopus cocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- SUBCRELULAR LOCATION: Type I membrane protein (Potential).
-:- TISSUB SPECIFICITY: Selectively present in the distal parts nephron (medhulary and papillary collecting ducts and end postilary collecting ducts and end post cortical collecting tubule) and in the epithelial cells of distal colon. No expression is found in renal proximal tubul loop of henle and distal tubule, proximal colon, small inter lung, choroid plexus, salivary glands, or brain.
-:- INDUCTION: By corticosteroids.
-:- SIMILARITY: Belongs to the FXXD family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a colbetween the Swiss Institute of Bioinformatics and the EMBL outhe European Bioinformatics Institute. There are no restrictionse by non-profit institutions as long as its content is imposfied and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Re
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cellular localization and regulation of CHIF in kidney and colc
Am. J. Physiol. 271:C753-C762(1996).
-!- FUNCTION: Induces a potassium channel when expressed in xenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Last annotation update)
FXYD domain-containing ion transport regulator 4 precursor (Charinducing factor) (CHIF) (Corticosteroid-induced protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FXYD DOMAIN-CONTAINING ION TRANSPOR
                                                                                                                            1 MERVTLA-LLLLAGLTALEANDPFANKDDPFYYDWKNLOLSGLICGGLLAIAGI?
                                                                                                                                                                      1 MEEITCAFLLLLAGLPALEASDP-VDKDSPFYYDWESLQLGGLIFGGLLCIAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY.
MEDLINE-97000648; PubMed-8843704;
Capurro C., Coutry N., Bonvalet J.-P., Escoubet B., Garty H.,
                                    DB 1; Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PÉGN, PF02038, ATPIGI PLM WĀTB; 1.
PROSITE; PS01310; FXYD; 1.
Transmembrane; Signal; Ionic channel; Ion transport.
                               Score 276.5; DB 1
Pred. No. 1.7e-22;
8; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                   87 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation updat
                                                                                                                                                                                                                    60 KCKYKSSQKQHSPVPEKAIPLITPGSATTC 89
                                                                                                                                                                                                                                               60 KCKCRRTHKP-SSLPGKATPLIIPGSANTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIK, 139391; 139391.
[hterPro; IPR030272; ATP1G1 PLM MAT8.
                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
                               66.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUB=Colon;
TARA-TARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 141254; AAA74691.1; -.
PIR; 159391; 159391.
                                                                              60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 36, (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Farman N.;
                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
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                                                                                                                                                                                                                                                                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                         ROT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation-Bioinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial unires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S.,
Zawa M., Nishi K., Komno H., Adachi J., Fukuda S.,
zawa M., Nishi K., Toyosawa H., Kondo S., Yamanaka I.,
azaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
atsuda H.A., Ashburner M., Batalov S., Casavant T.,
W., Gaasterland T., Gissi C., King B., Kochiwa H.,
wis S., Marsuo Y., Nikaido I., Peeole G., Quackenbush J.,
vis S., Marsuo Y., Nikaido I., Peeole G., Quackenbush J.,
ido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
ffelli D., Bojunga N., Carninci P., de Bonaido M.F.,
J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
rchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
ato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
oyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
S.A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                  (Rel. 41, Last annotation update)
containing ion transport regulator 4 precursor (Channel tor) (CHIF).
                                                                                                                                                                                                                                                                                                                                                   letazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
theria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FXYD DOMAIN-CONTAINING ION TRANSPORT REGULATOR 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    390(2001).
390(2001).
Belongs to the FXYD family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL). 7EB0140941CFE926 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       channel; Ion transport.
                                                                                                                                             88 AA.
                                                                                                                                                                                                               Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uence of mouse CHIF (FXYD4),";
KSSQKQHSPVPEKAIPLITPGSATTC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R000272; ATPIGL PLM MATB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /6J; TISSUE=Kidney;
5660; PubMed=11217851;
                                                                                                                                                                                       41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29; AAK51508.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; Ionic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38
59
88
9269 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAB31372.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1310; FXYD; 1
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LAR TY:

8 AA;

39 60 AA;

17 ġ

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Sweadner K.J., Rael E.,
"The FXYD gene family of small ion transport regulators or channe cDNA sequence, protein signature sequence, and expression.",
Genomics 68:41-56(2000)
-!- FUNCTION: Induces a hyperpolarization-activated chloride curr
                        activating endogenous cocyte channels.
--- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
--- TISSUE SPECIFICITY: Expressed in a subset of murine breast to --- MISCELLANEOUS: Marker of a cell type preferentially transform
                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a coll between the Swiss Institute of Bioinformatics and the EMBL out the Buropean Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for centities requires a license agreement (See http://www.isb-sib.ch/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MERVILALL-LLAGLIALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MQEVVLSLLVLLAGLPTLDANDP-ENKNDPFYYDWYSLRVGGLICAGILCALGIIV
        when expressed in xenopus oocytes. May be a modulator capable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01311; FXYD; 1.
Transmembrane; Signal; Ionic channel; Chloride channel; Chloride;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FXYD DOMAIN-CONTAINING ION TRANSPORT REGULATOR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           when expressed in xenopus oocytes. May be a modulator capable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FXYD domain-containing ion transport regulator 3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Lee N.H., Glode, A., Chandra I., Mason T.M., Quackenbush
Kerlavage A.R., Adams M.D.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
RECONSTRUCTION FROM ESTS, AND CONCEPTUAL TRANSLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9CD61684B856E35D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 241.5; DB 1
Pred. No. 8.5e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 AA
                                                                                                             neu or ras oncoprotein.
-!- SIMILARITY: Belongs to the FXYD family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 KCKYKSSQKQHSPVPEKAIPLITPGSATTC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 KCKCKFROKP-SHRPGEGPPLITPGSAHNC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                    EMBL, BC002039, AAH02039.1, -.
PIR, S61552, S61552.
MGD, MG1:107497, Fxyd3.
InterPro, IPR003272, ATP1G1 PLM MATB.
Pfam, PF02038, ATP1G1 PLM MATB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 57.8%;
Matches 52; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 AA; 9526 MW;
                                                                                                                                                                                                                                                                                                                                                     EMBL; X93038; CAA63606.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 5 8
8 8 8
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88
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39
60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
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        à
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Lollins F.S., Wagner L., Shenmen C.M., Schuler G.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Jordan H., Morer T., Max S.I., Wang J., Hsieh F., Jordan H., Morer T., Max S.I., Wang J., Hsieh F., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Jullano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Swan P.J., McKernan K.J., Malek J.A., Gunsarane P.H., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., conserved B., Schenan M., Madan A., Rodrigues S., Sanchez A., and A., Young A.C., Shevchenko Y., Bouffard G.G., Touchman J.W., Green E.D., Dickson M.C., Grimwood J., Schulutz J., Wyers R.M., Schilus D.E., Schilus M.I., Skalska U., Smallus D.E., Schein J.E., Jones S.J.M., Marra M.A., Hallital analysis of more than 15,000 full-length se CDNA sequences ";
                                                                                                                                                                        TLA-LLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59
                                                                                                                                                                                                                   TCAFLLVLAGLPVLEANGP-VDKGSPFYYDWESLÓLGGMIFGGLLCIAGIAMALSG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184; Pubmed=7836447;
, Moorman J.R., Kowdley G.C., Kobayashi Y.M., Jones L.R.,
                                                                                                                                  7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rel. 42, Last annotation update)
ontaining ion transport regulator 3 precursor (Chloride
nducer protein Mat-8) (Mammary tumor 8 kDa protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phospholemman-like protein expressed in human breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Induces a hyperpolarization-activated chloride current
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cazoa; Chordata; Craniata; Vertebrata; Euteleostomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               initiate murine mammary tumors that share genetic ally absent in c-myc and int-2-initiated tumors."; 17-3426(1994)
                                                                                       DB 1; Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s a chloride conductance in Xenopus oocytes."; 270:2176-2182(1995).
                                                                                                                               17; Indels
POTENTIAL,
CYTOPLASMIC (POTENTIAL).
SDODEIFFC6B1BCCA CRC64;
                                                                                     Score 256.5; DB 1; Pred. No. 2.2e-20; 11; Mismatches 17
                                                                                                                                                                                                                                                           KSSQKQHSP--VPEKAIPLITPGSATT 88
                                                                                                                                                                                                                                                                                                                                                                                                                 88 AA
                                                                                                                                                                                                                                                                                                      -- CRRNHTPSSLPEKVTPLITPGSAST 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=7970700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rel. 36, Created)
                                            9084 MW;
                                                                                       55.6%;
                                                                                                           61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Breast;
                                                                                                                             onservative
                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leder P.;
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Rel. 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR PLML.
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1-like) (Mouse)

1060

797;

(e) 8

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Length 88; 24; Indels i

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TISSUE-Drinary bladder;

X MEDINE=22388257; PubMed=12477932;

A Strausberg K.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Hopkins R.P., Jordan H., Bonaldo M.F., Casavant T.L., Scheetz

B Kapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
FXYD domain-containing ion transport regulator 3 precursor (Chlc conductance inducer protein Mat-8) (Mammary tumor 8 kDa protein)
                                                              EMBL; AB015759; BAA35078.1; -.
InterPro; IPR000272; ATPLG1 PLM MAT8.
Pfam; PF02038; ATPLG1 PLM MĀT8.
PROSITE; PS01310; FXYD; 1.
Transmembrane; Signal; Ionic channel; Chloride channel; Chloride
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morrison B.W., Moorman J.R., Kowdley G.C., Kobayashi Y.M., Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Mat-8, a novel phospholemman-like protein expressed in human br tumors, induces a chloride conductance in Xenopus occytes.";
                                                                                                                                                                                                                                                                                       FXYD DOMAIN-CONTAINING ION TRANSPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MERVILA-LLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 230.5; DB 1; Length 88; Pred. No. 1.2e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lei W., Wu M.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL) 6CC7810B90512E5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 KCKYKSSQKQHSPVPEKAIPLITPGSATTC
               or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 270:2176-2182(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Breast;
MEDLINE=95138184; PubMed=7836447;
                                                                                                                                                                                                                                                                                                                                            38
59
88
9314 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                           17
88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FXYD3 OR MATS OR PLML.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Lung carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       88 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                       18
                                                                                                                                                                                                                                                                                                                                                  3.9
60
                                                                                                                                                                                                                              Ion transport.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leder
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                                                                                                                ROT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation—Bioinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial uires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTLALL-LLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
containing ion transport regulator 3 precursor (Chloride inducer protein Mat-8) (Mammary tumor 8 kDa protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Induces a hyperpolarization-activated chloride current ressed in xenopus oocytes. May be a modulator capable of mg endogenous oocyte channels.
LAR LOCATION: Type I membrane protein (Potential).
TY: Belongs to the FXYD family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of P-type transporting ATPases and chromosomal locations es.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FXYD DOMAIN-CONTAINING ION TRANSPORT REGULATOR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       etazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
theria, Cetartiodactyla, Suina, Suidae, Sus.
ng endogenous oocyte channels.
LAR LOCATION: Type I membrane protein (Potential).
TY: Belongs to the FXYD family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL). 45AFE872FD1AF944 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal; Ionic channel; Ion transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 234.5; DB ]
Pred. No. 4.6e-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKSSQKQHSPVPEKAIPLITPGSATTC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CKFSQKP-SHRPGDGPPLITPGSAHNC 88
                                                                                                                                                                                                                                                                                                       mail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                            65; -; NOT ANNOTATED CDS.
R000272; ATP1G1_PLM_MATB.
8; ATP1G1_PLM_MATB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Funct. 23:315-323(1998).
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STANDARD;

mucosa;

M.N.A

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Conservative

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AA;

1310; FXYD;

OT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation—Bioinformatics Institute. There are no restrictions on its profit institutions as its content is in no way this statement is not removed. Usage by and for commercial ires a license agreement (See http://www.isb-sib.ch/announce/ ECIFICITY: Expressed in a subset of human breast tumors. EOUS: Marker of a cell type preferentially transformed by ton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., adan A., Young A.C., Shevchenko Y., Bouffard G.G., .., Touchman J.W., Green E.D., Dickson M.C., .., Kraymwood J., Schmutz J., Myers R.M., Schwinski M.I., Skalska U., Smailus D.E., Schein J.E., Jones S.J.M., Marra M.A., an initial analysis of more than 15,000 full-length essed in xenopus oocytes. May be a modulator capable of g endogenous oocyte channels.

AR LOCATION: Type I membrane protein (Potential). se CDNA sequences."; cad. Sci. U.S.A. 99:16899-16903(2002).
Induces a hyperpolarization activated chloride current Y: Belongs to the FXYD family. ail to license@isb-sib.ch). oncoprotein.

Signal; Ionic channel; Chloride channel; Chloride; C:integral to plasma membrane; TAS. F:chloride channel activity; TAS. 1; P:chloride transport; TAS. 000272; ATP1G1 PLM MAT8. AAA73922.1; -. ; AAH05238.1; -. CAA63604.1; -. 310; FXYD; 1 027; FXYD3.

CYTOPLASMIC (FOTENTIAL).
MISSING (IN REF. 2).
S -- S SEWRSSGEOAGRGWGSPPLTTQLSFTG (IN REF. 2). FXYD DOMAIN-CONTAINING ION TRANSPORT EXTRACELLULAR (POTENTIAL). 6D674D668EB32493 CRC64; POTENTIAL. 9263 MW; 38 59 87 58 20

muscle contraction.

Gaps 'n 46.5%; Score 214.5; DB 1; Length 87; 24; Indels ; Pred. No. 5.9e-16; 11; Mismatches 24 54.58; onservative

4;

LLALLL - LAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSG 59 TIGLIVFLAGFPVLDAND-LEDKNSPFYYDWHSLQVGGLICAGVLCAMGIIIVMSA 59

KSSOKO-HSPVPEKAIPLITPGSA 86 <FGQKSGHH--PGETPPLITPGSA 85</pre>

92 AA. STANDARD;

Waaseeee

Rel. 36, Created)
Rel. 41, Last sequence update)
Rel. 42, Last annotation update)
precursor (FXYD domain-containing ion transport

TISSUB-Brain, Lung, and Testis;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.I.

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Eonaldo M.F., Casavant T.L., Scheetz I.

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.

Bosak S.B., McEwan P.J., McKernan R.J., Malek J.A., Gunaratne F.F.

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.

Fahey J., Helton E., Ketteman M., Maden A., Rodrigues S., Sanchez

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,

Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;

Hogenstation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Induces a hyperpolarization-activated chloride curr
when expressed in xenopus oocytes. May have a functional role TISSUE=Heart;
MEDLINE=27312702; PubMed=9169143;
Chen L.-S.K., Lo C.F., Numarn R., Cuddy M.;
Characterization of the human and rat phospholemman (PLM) cDNAs localization of the human PLM gene to chromosome 19q13.1."; Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. MEDIJNE=20408885; PubMed=10950925; Sweadner K.J., Rael E.; "The FXYD gene family of small ion transport regulators or ch CDNA sequence, protein signature sequence, and expression."; Genomics 41:435-443(1997) Genomics 68:41-56(2000). Homo sapiens (Human) SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. NCBI_TaxID=9606;

-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Highest expression in skeletal muscle and heart. Moderate levels in brain, placenta, lung, liver, panor uterus, bladder, prostate, small intestine and colon with muclining. Very low levels in kidney, colon and small intestine without mucosa, prostate without endothelial lining, spleen, -!- PTM: Major plasma membrane substrate for camp-dependent prote kinase (PK-A) and protein kinase C (PK-C) in several differen tissues (By similarity). Phosphorylated in response to insuli adrenergic stimulation. This SWISS-PROT entry is copyright. It is produced through a coll between the Swiss Institute of Bloinformatics and the EMBL out the European Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch/or send an email to license@isb.sib.ch/). -! - SIMILARITY: Belongs to the FXYD family. EMBL; BC032800; AAH32800.1; -. EMBL; U72245; AAC51286.1; testis.

Genew; HGNC:4025; FXYDI. MIM; 602359; -.

MIM; 602359; -. GO; GO:0005887; C:integral to plasma membrane; TAS.

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CYTOPLASMIC (POTENTIAL).
PHOSPHORYLATION (BY PKC AND PKA) (I
                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (BY PKA) (BY SIMIL! 890DE301BF8E740A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi
Mammalia; Eutheria; Rođentia; Sciurognathi; Muridae; Murinae; Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a col between the Swiss Institute of Bioinformatics and the EMBL ou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 LLLLAG-LTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamaguchi F., Yamaguchi K., Tai Y., Sugimoto K., Tokuda M.;
"Molecular cloning and characterization of a novel phospholemmar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q91XV6; Q9JLR4;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
FXYD domain-containing ion transport regulator 6 precursor (Vaseddothelial cell specific protein 6) (VESP6) (Phosphohippolin)
FXYD6 OR PHP.
      entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein from rat hippocampus.";
Brain Res. Mol. Brain Res. 86:189-192(2001).
-!- SUBCELLUTAR LOCATION: Type I membrane protein (Potential).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aoki T., Toyoda H., Nishimoto S., Tawara J., Komurasaki T., "Identification of VESP6, a vascular endothelial cell specific
                                                                                                                                                                                                                                                                                                                                                                                                 Score 126.5; DB 1; Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                          23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                           Transmembrane; Phosphorylation; Signal; Ionic channel;
Chloride channel; Chloride; Ion transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 1.2e-06; 15; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 AA.
                                                                                                                                                                                                                          PHOSPHOLEMMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Sprague-Dawley; TISSUE=Hippocampus; MEDLINE=21105932; PubMed=11165386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the FXYD family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sold=Q91XV6-2; Sequence=VSP_001586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q91XV6-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                                                                               POTENTIAL
                                                             EMBL; M63934; -; NOT ANNOTATED CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                               PIR; A40533; A40533.

InterPro; IRRO0272; ATPLG1 PLM
Pfan; PF02038; ATPLG1 PLM
AATB;
PROSITE; PS01310; FXYD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                          10500 MW;
                                                                                                                                                                                                                                                                                                                                                                                                   27.48;
                                                                                                                                                                                                                                                                                                                                                                                                                        41.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                          29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                          92
92
93
93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 ÓQÓRTGEPDE 75
                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                          92 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
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21
36
57
83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.";
                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                 MOD_RES
                                                                                                                                                                                                                                                                                                                                        MOD RES
                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FXY6_RAT
      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation-Bioinformatics Institute. There are no restrictions on its profit institutions as long as its content is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEANDPFANKDDPFYYDWKNLQLSGLIAIAGIAAVLSGKCKYKSSQKQHSPV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scott B.T., Jones L.R.; n and complete sequence determination of the major plasma strate for cAMP-dependent protein kinase and protein
                                                                                                                                                                                                                                                                                                                                                                                                                 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Induces a hyperpolarization-activated chloride current ressed in xenopus cocytes. May have a functional role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aorta,
brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or plasma membrane substrate for camp-dependent protein PK-A) and protein kinase C (PK-C) in several different Phosphorylated in response to insulin and adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                              ie; Phosphorylation; Signal; Ionic channel; Innel; Chloride; Ion transport.

21 20 BY SIMILARITY.
21 35 PHOSPHOLEMMAN.
21 35 EXTRACELLULAR (POTENTIAL).
36 56 POTENTIAL.
57 CYTOPLASMIC (POTENTIAL).
83 89 PHOSPHORYLATION (BY PKC AND PKA).
88 89 PHOSPHORYLATION (BY PKC).
3 3 5 -> P (IN REF. 1).
5 G -> H (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAR LOCATION: Type I membrane protein.
PECIFICITY: Present in heart, esophagus, stomach, muscle, smooth muscle, and liver but absent from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tel. 36, Last sequence update)
tel. 41; Last annotation update)
precursor (FXYD domain-containing ion transport
                                                                                                                                                                                                                                                                                                                                                                       28.0%; Score 129; DB 1; Length 92; 41.3%; Pred. No. 6.5e-07; ive. 15; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                  11602EFEAFFD8BD8 CRC64;
154; F:chloride channel activity; TAS. 121; P:chloride transport; TAS. 136; P:muscle contraction; TAS. 18000272; ATPIGI_PLM_MATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TY: Belongs to the FXYD family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.A., AND SEQUENCE OF 21-92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266:11126-11130(1991).
                                                                           PLM MAT8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0422; PubMed=1710217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                    10441 MW;
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myocardium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ontraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aris (Dog)
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75

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Matches
       Bioinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial ires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60; PubMed=11217851; nagawa A., Yoshino M., Itoh M., Ishii Y., ara A., Shibata K., Yoshino M., Itoh M., Ishii Y., ara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., awa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Zaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., tsuda H.A., Ashburner M., Batalov S., Casavant T., Gasterland T., Gissi C., King B., Kochiwa H., is S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Staubli F., Szuki R., Tomita M., Wagner L., Washio T., Chili D., Bojunga N., Carninci P., de Bonaldo M.F., J., Bult C., Fletcher C., Fujita M., Gariboldi M., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
                                                                                                                                                                                                                                                                                                                                                                                                          TLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 60
                                                                                                                                                                                                                                                                                                                                                                                                                          gene expressed in the nervous system.";
                                                                                                                                                                                                                                                                                                                                                                               3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rel. 41, Created)
Rel. 41, Last sequence update)
Rel. 41, Last annotation update)
ontaining ion transport regulator 6 precursor (PLM-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                     FXYD DOMAIN-CONTAINING ION TRANSPORT REGULATOR 6.
                                                                                                                                                                                                                                                                                                                                                    27.0%; Score 124.5; DB 1; Length 94;
                                                                                                                                                                                                                                                                                                                                                                37.5%; Pred. No. 2e-06; ive 15; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL). Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                    1C0D35FA0C572451 CRC64;
                                                                                                                                                            Signal; Ionic channel; Ion transport;
                                                                                                                                                                                                                                                                                         /FIId=\overrightarrow{VSP} 001586.
N -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oba R., Kato K., Matsubara K.;
like ion channel gene expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSOKOHSPVPEKA--IPLITPGSA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FNOKPRAPGDEEAQVENLITINAA 87
                                                          to license@isb-sib.ch).
                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.A. (ISOFORMS 1 AND 2).
                                                                                                9; AAF66613.1; -.
300272; ATP1G1 PLM MATB.
; ATP1G1_PLM_MAT8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N.A. (ISOFORM 1).
                                                                                     8; BAB62242.1; -.
                                                                                                                                                                                                                                                                                                                     10388 MW;
                                                                                                                                                                                                                                                                                                                                                                                onservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                 ; ATP1G1_PI
310; FXYD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Q9CXD0;
                                                                                                                                                                                                      94
                                                                                                                                                                          icing.
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PERGUENCE FROM N.A. (ISOFORMS 1 AND 2).

STRAIN=FVB/N; TISSUE-Brain;

MEDLINE=2238B257; PubMed=12477932;

MEDLINE=2238B257; PubMed=12477932;

MEDLINE=2238B257; PubMed=12477932;

MEDLINE=2238B257; PubMed=12477932;

MEDLINE=2238B257; PubMed=12477932;

MA Altschul S.F., Zeeberg B., Buetow K.H., Schemfer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F., Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T. Brownstein M.J., Usdin T.B., Peres G.J., Abramson R.D., Mullahy E. Raha S.S., Loquellano N.A., Peres G.J., Abramson R.D., Mullahy E. Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.F. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk E. Millalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk E. Milling M., Madan A., Rodrigues S., Sanchez, M. Milling M., Madan A., Rodrigues S., Sanchez, M. Hulton E., Ketteman M., Madan A., Rodrigues S., Sanchez, Blakesley R.W., Tucuchman W., Green E.D., Dickson M.C., Rhetzeffeld Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences ";

Proc. Interpretation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences ";

Proc. Nall. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- ALTERNALIVE PRODUCTS: Type I membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      o.
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato. K., Schoenbach C., Seya T., Shibata Y., Storch K. Suzuki H., Toyo-oka K., Wang K.H., Weliz C., Whittaker C., Wilmir Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a coll between the Swiss Institute of Bioinformatics and the EMBL out the Buropean Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is ir modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FXYD DOMAIN-CONTAINING ION TRANSPORT REGULATOR 6. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                            Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Match 26.8%; Score 123.5; DB 1; Length 94; Local Similarity 37.5%; Pred. No. 2.5e-06; es 33; Conservative 15; Mismatches 37; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
Missing (in isoform 2).
/FTId=VSP_001585.
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EMBL; AK018354; BAB31174.1; -...
EMBL; BC042579; AAH52579.1; -...
MGD; MGI:1890226; Fxyd6.
InterPro; IPR000272; ATPEGI PLM MAT8.
Pfam; PR02038; ATPIGI PLM MAT8.
PROSITE; PS01310; FXYD; 1...
Transmembrane; Signal; Ionic channel; Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q9D164-2; Sequence=VSP 001585;
-!- SIMILARITY: Belongs to the FXYD family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q9D164-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB032010; BAB40451.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 AA; 10374 MW;
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SIGNAL
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35
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DOMAIN
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(Mouse)

M N.A.

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-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- PTM: Major plasma membrane substrate for camp-dependent prot kinase (PK-C) and protein kinase (PK-C) in several differe tissues. Phosphorylated in response to insulin and adrenergi stimulation (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ra
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen L.-S.K., Lo C.F., Numann R., Cuddy M.; "Characterization of the human and rat phospholemman (PLM) cDNAs localization of the human PLM gene to chromosome 19q13.1."; Genomics 41:435-443(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sweadner K.J., Rael E.; "The FXYD gene family of small ion transport regulators or chann
                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY PKA) (BY SIMILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LALCVCLLSMASABAPQEP----DPFTYDYHTLRIGGLTIAGILFILGILIILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- FUNCTION: Induces a hyperpolarization-activated chloride cur when expressed in xenopus oocytes. May have a functional rol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 VTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a col
                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (BY PKC AND PKA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phospholemman precursor (FXYD domain-containing ion transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA sequence, protein signature sequence, and expression."; Genomics 68:41-56(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 115.5; DB 1; Length 92; Pred. No. 1.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Mismatches 26; Indels
                EMBL; AF091390; AAD11781.1; -.
EMBL; AF089734; AAD41683.1; -.
EMBL; AK002565; BAB22208.1; -.
EMBL; AK01:1889273; Fxyd1.
InterPro; IPR000272; ATP1G1 PLM MAT8.
PFGMT; PS01310; FXPJ; 1.
Transmembrane; Phosphorylation; Signal; Ionic channel;
Chloride channel; Chloride; Ion transport.
                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                  OBDB1DC83417F3AD CRC64;
                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 AA.
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                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                           PHOS PHOLEMMAN
                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=20408885; PubMed=10950925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97312702; PubMed=9169143;
                                                                                                                                                                                                                                                                                                                                                                                                                                              25.1%;
34.2%;
                                                                                                                                                                                                                                                                                                                                                                                                  10323 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :|:| : |::
63 KFNQQQRTGEPDE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 KSSQKQHSPVPEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscle contraction.
                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  92 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           21
21
36
57
83
                                                                                                                                                                                                                                                                                                                                                                             88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulator 1).
FXYD1 OR PLM.
                                                                                                                                                                                                                                                                                     TRANSMEM
DOMAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                             MOD RES
                                                                                                                                                                                                                                         CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  008589
                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLM_RAT
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à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /61; TISSUE=Kidney;
56(6); PubMed=11217851;
Inagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Inagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Zawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
azaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
atsuda H.A., Ashburner M., Batalov S., Casavant T.,
W., Gasterland T., Gissi C., King B., Kochiwa H.,
wis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Staubil F., Suzuki R., Tomita M., Wagner L., Washio T.,
ido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
ifelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
J., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
rchionni L., Mashima J., Mazzarelli J., Mombacrts P.,
Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
ato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
oyo-oka K., Wang K.H., Weitz C., Whithaker C., Wilming L.,
s.A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                VTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK 60
                                                Induces a hyperpolarization-activated chloride current ressed in xenopus oocytes. May have a functional role in ontraction (By similarity).

LAR LOCATION: Type I membrane protein.

or plasma membrane substrate for camp-dependent protein PK-A) and protein kinase C (PK-C) in several different phosphorylated in response to insulin and adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                            etazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
theria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3265; PubMed=11410367;
Jia L.G., Kobayashi Y.M., Palmer C.J., Mounsey J.P.,
, Jones L.R., Tucker A.L.;
ure and expression of phospholemman in mouse.";
79(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                        (Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
n precursor (FXYD domain-containing ion transport
                                                                                                                                                                                                                                                              92 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TY: Belongs to the FXYD family.
                                                                                                                                               87
                                                                                                        KSSQKQHSPVPEKA--IPLITPGSA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to license@isb-sib.ch).
                                                                                                                                               SFNOKPRAPGDEEAQVENLITINAA
                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ion (By similarity)
                                                                                                                                                                                                                                                                                                        (Rel. 41, Created)
                                                                                                                                                                                                                                                         STANDARD;
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SOSSIONAL AND SOURCE SO

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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy Bosak S.A., McBwan P.J., McKernan K.J., Amlek J.A., Gunaratne P. Richards S., Worley K.C., Halle S., Garcia A.M., Gay L.J., Fulyk Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Rodrigues S., Sanche Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S. M., KIZywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.; Length M. C. Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sodium/potassium-transporting ArPase gamma chain (Sodium pump gan chain) (Na+/K+ ArPase gamma subunit) (FXYD domain-containing ion transport regulator 2).

FXYDS OR ATPIG OR ATPIG.

Bos taurus (Bovine).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collective the Swiss Institute of Bioinformatics and the EMBL outles Bushean Bioinformatics Institute. There are no restrictionse by non-profit institutions along as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FXYD DOMAIN-CONTAINING ION TRANSPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LALLLLAGLTALEANDPFANKD --- DPFYYDWKNLQLSGLICGGLLAIAGIAAVL
                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- SIMILARITY: Belongs to the FXYD family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 112.5; DB 1; Length 95; Pred. No. 3.7e-05; 14; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
CYTOPLASMIC (POTENTIAL).
3F083146A42422CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000272; ATPIGI PLM MAT8.
Pfam; PF02038; ATPIGI PLM MĀT8; 1.
PROSITE; PS01310; FXYD; 1.
Transmembrane; Signal; Ionic channel; Ion transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-00T-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGULATOR
                                                                                                                                                                                                                                                                                                                                                       human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL136699; CAB66634.1; -.
EMBL; BC018652; AAH18652.1; -.
Genew; HGNC:4030; FXYD6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 CSFNOKPRAPGDEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
95
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58
95
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NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19
36
59
95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 606683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATNG BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q04645;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
                 RRAPA RRAPA PRAPA 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Swiss Institute of Bioinformatics and the EMBL outstation-Bioinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial likes a license agreement (See http://www.isb-sib.ch/announce/aail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CVCLLSMASAEA----PQEPDPFTYDYHTLRIGGLTIAGILFILGILIILSKRCRC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257; PubMed=12477932; L., Feingold E.A., Grouse L.H., Derge J.G., L., Foligold E.A., Grouse L.H., Derge J.G., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
PHOSPHORYLATION (BY PKC AND PKA) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                917; PubMed=11230166;
eil B., Wellenreuther R., Gassenhuber J., Glassl S.,
oecher M., Bloecker H., Bauersachs S., Blum H.,
esterhoeft A., Beyer A., Koehrer K., Strack N.,
ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
orn B., Klein M., Poustka A.;
talog of human genes and proteins: sequencing and
00 novel complete protein coding human cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ontaining ion transport regulator 6 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 113; DB 1; Length 92; Pred. No. 3.2e-05; 18; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                 Phosphorylation; Signal; Ionic channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPG -> PLH (IN REF. 1).
IAGI -> AGIL (IN REF. 1)
29530D084B3CB7C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41, Last sequence update)
42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY
PHOSPHOLEMMAN
                                                                                                                                                                                                                                                                                                                                         nnel; Chloride; Ion transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                            1000272; ATPIGI PLM MAT8.

3; ATPIGI PLM MAT8; 1.

1310; FXYD; 1.
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Rel. 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tazoa; Chordata;
heria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46
10365 MW;
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OORTGEPDE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KOHSPVPEK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          onservative
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56
92
83
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PROT entry is copyright. It is produced through a collaboration sowiss Institute of Bioinformatics and the EMBL outstation - Bioinformatics and the EMBL outstation - 10 Bioinformatics Institute. There are no restrictions on its 1-profit institutions as long as its content is in no way it this statement is not removed. Usage by and for commercial juines a license agreement (See http://www.isb-sib.ch/announce/mmail to license@isb-sib.ch).
                                       Blemesucite, D., Lilly State and immunological characterization of the gamma a small protein associated with the Na,K-ATPase."; I. 21:579-586(1991) forming the receptor site for cardiac le binding or may modulate the transport function of the
                                                                                                                                                                                                                                                                                                                JIAR LOCATION: Type III membrane protein (Potential).
SPECIFICITY: Highest levels expressed in the kidney and
Restricted to the basolateral membrane in renal epithelial
d varies in its level of expression along the nephron.
ITY: Belongs to the FXXD family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                          Composed of three subunits: alpha (catalytic), beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKSSQKQHSPVPEKAI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
20.9%; Score 96.5; DB 1; Length 58; 34.6%; Pred. No. 0.0011; tive 14; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 39 POTENTIAL.
38 AA; 6545 MW; 54B590B816731183 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ssium transport; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , D46435.
PR000272; ATPIGL PLM MATB.
38; ATPIGL PLM MATB; 1.
01310; FXYD; 1.
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193 (1)

66 14.3 446 17 Q97UY7 65.5 14.2 88.4 4 Q8NBP9 65.5 14.2 1185 16 Q8EGS8 65.1 14.2 1185 16 Q8EGS8 65.1 14.1 327 10 Q9LVG3 65 14.1 760 13 Q90638 64.5 14.0 15 11 Q9R126 64.5 14.0 455 17 Q8EXS 64.5 14.0 550 12 Q9CEW9 64.5 14.0 550 12 Q9CEW9 64.5 14.0 550 12 Q9CEW9	30 64 13.9 315 10 Q9LSS8 Q9jiss8 arg	RESULT 1 QBETD2 ID QBETD2 DT 01-MAR-2003 (TrEMBLrel. 23, Created) DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) OC Mus musculus (Mouse). OC Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus NN [1]		Query Match Best Local Similarity 29.5%; Pred. No. 0.04; Matches 23; Conservative 14; Mismatches 35; Indels 6; (Qy 11 LAGLTALEANDFANKDDFYYDWKNLQLSGLIGGGLLAIAGIAAVLSGKCK-YKE: Db 1 MATPTGSPTNVPEETDPFFYDYATVQTVGWTLATIMFVLGIIILSKKVKCRKZQY 70 HSPVPEXAIPLITPG 84 Db 59 ESPTCKSCKSELPSSAPG 76 RESULT 2 RESULT 2
sion 5.1.6 004 Compugen Ltd. del 40 ; Search time 36 Seconds (without alignments) 637.963 Million cell update	PREVILABLIFACE STATE BY LOSUM62 JOSUM62 PROP 10.0 , Gapext 0.5 10525 seqs, 258052604 residues LS satisfying chosen parameters: 830525 19th: 0 19th: 200000000 1inimum Match 0% 1aximum Match 100% 1isting first 45 summaries	<pre>sp_arches:* sp_barceria:* sp_fungi:* sp_invertebrate:* sp_invertebrate:* sp_mammal:* sp_mammal:* sp_pagarelle:* sp_plant:* sp_plant:* sp_plant:* sp_virus:* sp_virus:* sp_unclassified:* sp_urclassified:* sp_archeap:*</pre>	an or equal to the score of the resilan or equal to the score of the resily analysis of the total score districtions of the to	had caemo caemo caemo bac yers yers yers arah parah parah bomo bomo stre shev

177

PRT;

PRELIMINARY;

(TrEMBLrel. 23, C (TrEMBLrel. 23, I (TrEMBLrel. 23, I

Metazoa; Chordata; Itheria; Primates;

M N.A

(Human)

382; AA013166.1;

Conservative

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Nakashima N., Koizumi M., Watanabe H., Hiroaki N.;
"Complete nucleotide sequence of the Nilaparvata lugens recviru:
putative member of the genus Fijivirus.";
J. Gan. Virol. 77:139-146(1996).
EMBL; D49696; BAA08545.1;
Interpror, IPROO2877; FtsJ.
Fram: PPRO1228; FtsJ.
SEQUENCE 1132 AA; 130041 MW; GEBF5714B8EA0576 CRC64;
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--DLGGIFSGIGGMLGSIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 LLAGLTALEANDPFANKDDPFYYDWKN----LQLSGLICGGLLAIAGIAAVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.8%; Score 73; DB 12; Length 1132; 28.6%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                 viruses; Reoviridae; unclassified Reoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
NCBI_TaxID=1423,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Lapidus A., Galleron N., Sorokin A., Ehrlich D.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                   ., Takao J., Das A., Cruz P.D. Jr., Ariizumi K.; ion of genes for secreted and membrane-anchored proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                letazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Peloderinae; Caenorhabditis.
                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ence of the nematode C. elegans: a platform for
ig biology. The C. elegans Sequencing Consortium.";
2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.9%; Score 73.5; DB 5; Length 196; 30.7%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----NKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.2%; Score 84; DB 4; Length 178; 40.4%; Pred. No. 0.13; Live 7; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e of C. elegans cosmid F49F1."; or-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                     :ytes.";
)CT-2002) to the EMBL/GenBank/DDBJ databases.
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156; AAF99970.1; -.
1F1.3; CE25894.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .78 AA; 19313 MW; 8129C0AD3A449584 CRC64;
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                                                              (TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
38 associated transmembrane protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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                                              Created)
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20.5 kDa protein.

elegans.

M N.A.

amsley P.;

M N.A.

PRELIMINARY;

Conservative

protein.

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M N.A.

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SEQUENCE
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laser P., Goffeau A., Golightly E.J., Grandi G.,
Gyy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
ramata D., Kasahara Y., Klaerr Blanchard M., Tones L.,
randtanois S., Laubar B., Kumano M.,
apidus A., Laidinois S., Laubar J., Lazarevic V.,
vine A., Liu H., Masuda S., Mauel C., Medigue C.,
allado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
hl T.M., Porteelle D., Porvollik S., Prescott A.M.,
Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
ivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
nlan E., Schleich S., Schroeter R., Scoffone F.,
Sekowska A., Seror S.J., Serror P., Shin B.S.,
Taconi E., Takahashi H., Takemaru K.,
Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
chiyama S., Vandenbol M., Vannier F., Vassarotti A.,
nbutt R., Wedler E., Wedler H., Weitzenegger T.,
Aipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
foshikawa H.F., Zumstein B., Yoshikawa H., Danchin A.,
senome sequence of the gram-positive bacterium Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415; PubMed=11586360, Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Sebaihia M., James K.D., Churcher C., Mungall K.L., ham D., Bentley S.D., Churcher C., Mungall K.L., T., Cronin A., Davies R.M., Davis P., Dougan G., T., Cronin A., Davies R.M., Davis P., Dougan G., Hamlin M., Holroyd S., Jagels K., Karlyshev A.V., oule S., Oyston P.C.F., Quail M., Rutherford K., Skelton J., Scevens K., Whitehead S., Barrell B.G., nce of Yersinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             teobacteria, Gammaproteobacteria; Enterobacteriales;
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TrEMBLrel. 23, Last annotation update)
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Phosphate/phosphoenolpyruvate translocator protein-like.
Arabidopsis thaliana (Mouse-ear cress).
Musaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosi
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=KIMS / Biovar Mediaevalis;
MEDIINE=2137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Li
Perna N.T., Rose D.J., Mau B., Zhou S., Schwattz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner
                                                                                                                                                                                                                                 4 VTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGI-AAVI
                                                                                                                                                                                                                                                                 26 VTLAILILIAIRITIPINS------FFPW--VEKYGLTIGVLILTIGVMAPIA
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                                                                                                                                        15.0%; Score 69; DB 16; Length 150; 30.2%; Pred. No. 5.4; ive 14; Mismatches 32; Indels ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.0%; Score 69; DB 16; Length 157; 30.2%; Pred. No. 5.7;
                                                                  11 protein; Complete proteome.
150 AA; 15409 MW; B30184B6E99C5B9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 157 AA; 16330 MW; A7DBE45EFFD414F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
EMBL; AE013745; AAM84995.1; -
                                                                                                                                                                                                                                                                                                                               63 YKSSOKQHSPVPEKAIPLITPGSATT 88
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Nature 413:523-527(2001).
EMBL; AJ414155; CAC92299.1; -.
Pfam; PF04284; DUF441; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gamr
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                       26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 30.2%
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
                                                                                                                                                         Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=632;
                                                                     Hypothetical
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21; Indels

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MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

BMB., AE0061749, AAK03501.1.; -..

InterPro; IPR001807; Cl-channel volt.

Pfam, PF000654; voltage CLC, 1.

PRINTS; PR00762; CLCHANNEL.

Hypothetical protein; Complete proteome.

SEQUENCE 456 AA, 49349 MW; AA9C46DB68D4EDOA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinopterygii, Neopterygii, Teleostei; Euteleostei, Neoteleoste
Acanthomorpha; Acanthopterygii, Percomorpha; Perciformes;
Gobiesocoidei; Gobiesocidae; Arcos.
                                                                                    270 DWVVVLVSALLFADTKLTIINLFGYAIAIAGVAAYNNHKLKKEASKVVTTETPC
                                                          ---ICGGLLAIAGIAAVLSGKCKYKSSQ--KQHSP\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ERVTLALLLIAG--LTALEANDFF-----ANKDDFFYYDWKNLQLSGLIC---G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 ERRVLLGVLAAGFILVAIEGNNPYFPQYHGETSVPYLFLW--VSLCGVVCGFFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16; Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miya M.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pypothetical protein PM1417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
NADH dehydrogenase subunit 6.
                                                                                                                                                                                                                                                                     456 AA
   Pred. No. 16;
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.9%; Score 68.5; D:
29.7%; Pred. No. 22;
ive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23. Last som
                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Pm70;
MEDLINE=21145866; PubMed=11248100;
   29.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 LVKGLAGLSPSKIR 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 -IAGIAAVLSGKCK 62
                     20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 29.7
Matches 22; Conservative
                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                   330 LVSQGNTNT 338
                                                                                                                               80 LITPGSATT 88
                                                                                                                                                                                                                                                                                                                                                                                                 Pasteurella multocida
                                                        33 DWKNLQLSGL
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=181474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KU-149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arcos sp. KU-1'
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Muscle;
                                                                                                                                                                                                                                                                 Q9CL30
Q9CL30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8HKR3
                     Matches
                                                                                                                                                                                                                            RESULT 10
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                                                                                                                                                                                                                                             Q9CL30
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                                                                                                                                                                              analysis of Arabidopsis thaliana chromosome 3. I. Sequence the regions of 4,504,864 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Darninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Jnodera C.S., Palm C.J., Mrande M., Narusaka M.,
Jnodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
ski M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                            KNLQLSGL-------ICGGLLAIAGIAAVLSGKCKYKSSQ--KQHSPVPEKAIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N. N.A.

Jen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,

Jarninci P., Chang E., Dale J.M., Goldsmith A.D.,

Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,

M. Lin J., Miranda M., Narusaka M.,

Dnodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,

Ithwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,

Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
ta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                 . Kaneko T., Kato T., Asamizu E., Tabata S.; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                  DB 10; Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 340;
                                                                                                                                                                                                                                                                                                                                                                       21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s cDNA clones."; MG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4AR-2002) to the EMBL/GenBank/DDBJ databases.
286; AAK95272.1; -
729; AAM10353.1: -
                                                                                                                                                                                                                                                                                            339 AA; 37532 MW; 74FD50039AEE9F4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          785D5D610E5DFB86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 19, Last sequence update) (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                       15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340 AA.
                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                  14.9%; Score 68.5; 29.0%; Pred. No. 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.9%; Score 68.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .N21 19.
thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                           77480; PubMed=10819329;
                                                                                                                                                                                                                                                       220; BAB01046.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37509 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORF clones.";
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                         131-135 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQGNTNT 337
                                                   kamura Y.,
JAN-1999) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPGSATT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340 AA;
                                                                                                                                                                                                                                                                                                                                                     ilarity
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                                                                                                    OM N.A.
             OM N.A.
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2; BAC23785.1; -.

经过过程程度的证据

arity 30.2 Conservative

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SEQUENCE FROM N.A.

STRAIN=A3(2) / M145;

STRAIN=21996410; PubMed=12000953;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins I.
Croin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S.
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J..
                                                   01-MAR-2002 (TEBMBLrel. 20, Created)
01-MAR-2002 (TEBMBLrel. 20, Last sequence update)
01-MAR-2003 (TEBMBLrel. 23, Last annotation update)
Patched related protein translocated in renal cancer.
Homo sapiens (Human)
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MERVILALLLLAGLTALEANDPFANKDDPFYYDWK------NLQLSGLICGGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 LTRVTAQATVLMYILRM-----ANETDSFFISWDDFWDLICNLIISG--CDSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hopwood D.A.; "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.4%; Score 66.5; DB 16; Length 241; 28.4%; Pred. No. 18; tive 15; Mismatches 32; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bactèria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC21571, 1, --
INTERPO. IPR001841; Znf_ring.
Interpro; IPR001841; Znf_ring.
SMART; SM00184; NG; 1.
PROSITE; PS5049; ZF RING; 1.
PROSITE; PS5049; ZF RING; 2; 1.
Metal-binding; Zinc; Zinc-finger.
SEQUENCE 664 AA; 75993 MW; 9885F5915F019EF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-ORT-2003 (TrEMBLrel. 23, Last annotation update)
Purative ABC transport system integral membrane protein.
SC01257 OR 2SCG18.04C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 AA; 24559 MW; 300F70FACD254926 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
   664 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
14.6%; Score 67.5; 1
Best Local Similarity 28.6%; Pred. No. 43;
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 417:141-147(2002).
EMBL; AL939108; CAB99137.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 28.48
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :||:|
295 SAVISSVAHY 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 AAVLSGKCKY 63
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome
SEQUENCE 241 AA
                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coelicolor A3(2)
                                                                                                                                                                                                                                                                                                                                                              TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9K3I3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9K3I3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
Q9K3I3
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
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N
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"Y: CONTAINS I RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLALLLLAGLTALEANDPFANKDDPFYYDWK------NLQLSGLICGGLLAIAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                            eshima H., Endo H., Ishiguro N.B., Inoue J.G., Mukai T., (amaguchi M., Kawaguchi A., Mabuchi K., Shirai S.M.,
                                                                                                                                                               ins of higher teleostean phylogenies: A new perspective complete mitochondrial DNA sequences.", let. Evol. 26:121-138(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stazoa, Chordata, Craniata, Vertebrata, Buteleostomi, heria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1199; PubMed-9689122; West J.D., Boldog F., Tanaka N., Robinson L.J., i F., Drabkin H.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.6%; Score 67.5; DB 4; Length 664, 28.6%; Pred. No. 43; ive 11; Mismatches 24; Indels 1E
                                                                                                                                                                                                                                                                                                                                                                                     14.8%; Score 68; DB 8; Length 173; 30.2%; Pred. No. 8.3; Live 14; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                  1.
73 AA; 17892 MW; SFF3DL0C1CBF8A2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSEB6C925B5ED4D3 CRC64;
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1089; ZF_RING_2; 1. 1; Zinc; Zinc-finger. 14 AA; 76007 MW; 55

onservative

SSVAHY 304 SGKCKY 63

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#18

001841; Znf ring. '; zf-C3HC4; 1. 11; AAC39930.1; -.

664 AA.

PRT;

RELIMINARY;

(Human)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALPVPVIVSNFNYFYHRETEGEEQAQYMHVGSCQHLSSSAEELRKARSNSTLSKSEY 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKY 63
                          14.4%; Score 66.5; DB 6; Length 516;
larity 20.1%; Pred. No. 42;
Conservative 14; Mismatches 36; Indels 69; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          cuniculus (Rabbit).
etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M N.A.
ealand White;
9424,
9424,
Boulpaep B.L., Segal A.S., Desir G.V.;
loning of a glibenclamide sensitive, voltage-gated
expressed in rabbit kidney.";
set. 97:2525-2531(1996).
                                                                                                                                                                                                                                                                                             (TrEMBLrel. 01, Created)
(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
e-sensitive voltage-gated potassium channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Transmembrane.
16 Aa; 57430 MW; 795E84998BCA7CAA CRC64;
                                                                                                                      : ||::
RLSLAAVPQRGRWFAAKLAVIAVPALVVGLAT 114
                                                                                       QKQHSPVPEK------AIPLITPGSAT 87
                                                                                                                                                                                                                                                    516 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----HSPVPEKAIPLITPGSATTC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  k005210; BTB_POZ.

R005821; N+channel_pore.

R004050; K+channel_pore.

R004050; KV13channel.

R003059; Kv channel.

R003131; K_channel.

R003131; K_tetra.

R00372; Shaker_channel.

R00372; Shaker_channel.

4; K_tetra; 1.
                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        510; KV13CHANNEL.
491; KVCHANNEL.
496; SHAKERCHANEL.
                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25; BTB; 1.
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January 6, 2004, 16:04:06

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. - LD Community process HSPP-35 SEQ ID NO:35.
                   Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
      KW
                   inflammation; cardiovascular disease; anticancer; anti-inflammatory;
                 inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation, neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect; muscular dystrophy.
      KW
     KW
     KW
                   muscular dystrophy.
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     os
                  Homo sapiens.
    ХX
    PN
                 WO200000610-A2.
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    PD
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    ХX
                 25-JUN-1999;
                                                           99WO-US14484.
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    PR
                 26-JUN-1998;
                                                           98US-0090762
                 31-JUL-1998;
                                                           98US-0094983.
     ЯF
                 01-OCT-1998;
                                                          98US-0102686.
    PR
                 11-DEC-1998;
                                                         98US-0112129.
    ХX
                 (INCY-) INCYTE PHARM INC.
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                Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR; Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
   ΡI
   PΙ
   XX
                 WPI; 2000-160673/14.
   DR
                N-PSDB; AAZ98143.
   XX
                New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and
   РΤ
   РT
                cardiovascular disease
  PS
                Claim 1; Page 182; 327pp; English.
 XX
CC
CC
                AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
               human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
              numan signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, neuroprotective, cardiovascular and antiasthmatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagonists of HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular neurological
  CC
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            activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, reproductive or developmental disorders, (e.g. arteriosclerosis, cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, asthma, Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP nucleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diagnosis and monitoring), in gene therapy, as antisense, triplex-forming or ribozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping. HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and antagonists (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP-related diseases (in usual immunoassays), as therapeutic antagonists, in competitive drug screens, and for purification of HSPP from natural sources.
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            Sequence
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                                                                    100.0%; Score 461; DB 21; Length 89;
100.0%; Pred. No. 1.2e-50;
tive 0; Mismatches 0; Indels
    Best Local Similarity
    Matches
                               89; Conservative
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                              61 CKYKSSQKQHSPVPEKAIPLITPGSATTC 89
||||||||||||||||||||||||||||||||||61 CKYKSSQKQHSPVPEKAIPLITPGSATTC 89
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